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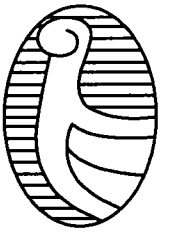

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THE VEGETATION OF THE MARSH MEADOW OF ZÁKÁNYSZÉK

A. Hagyó

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Abstract. The marsh meadow of Zákányszék is a valuable semi-natural grass. During its mapping survey ten protected plant species were found. The area contains marsh meadows and sand dunes uprising from them. The vegetation is mosaic-like in accordance with the variable microrelief. Among the valuable vegetation types of the area there are typical and transitional types as well. Altogether eleven vegetation units can be differentiated. Three of them are transitional ones that don't only cover transitional stripes but also extended areas. Numerical methods also validated these vegetation types.

Keywords: grasslands, indirect gradient analysis, marshes, numerical methods, vegetation mapping

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Introduction

In the southern Kiskunság Rapaics (1927) was the first to deal with the research of plant communities. Bodrogközy (1961) summarized the results of his habitat ecological researches made in the southern Kiskunság and described the plant communities. He made vegetation maps of many grasslands including the marsh meadow of Zákányszék. In the 1990s Gaskó (1995, manuscript) revealed the botanical values of numerous semi-natural grasslands in the southern Kiskunság and also gave recommendations for protection of some areas. The nearest area to the marsh meadow of Zákányszék which he recommended for protection is the Zákányi Basin that is north to it. Owing to his work and the realization of its preciousness the research of the grasslands of southern Kiskunság was started. Csete (1997) made the botanical description of the Ásotthalmi marsh meadow nature conservation area. With its 22 protected plant species this is the most valuable marsh meadow in the area. At the end of the 90s Margóczi *et al.* (1998) made coenological researches on more than 30 grasslands in the Dorozsma-Majsai-sand plateau geographical area. During their researches they found many grasslands including the marsh-meadow of Zákányszék with valuable vegetation and populations of protected plant species. They focused on two plant communities from the point of view of nature conservation, these are the *Succiso-Molinietum hungaricae* and the *Astragalo austriacae- Festucetum sulcatae* associations. They aimed to do further coenological researches on the grasses. In the D-TMap 1996-2000 project Margóczi (1998) made a habitat map of the sample area Nr. 35 that involves the marsh meadow of Zákányszék. She signed mostly a mosaic of *Succiso-Molinietum hungaricae*, sand-steppe meadow and salt-affected meadows, and some salt-affected marshes and sand-steppe meadow in the area of the marsh meadow of Zákányszék. Urbán (1999) carried out coenological and pedological researches on the sand-steppe meadow stands of some meadows (including the marsh meadow of Zákányszék) in the southern Kiskunság, Madarász (2000) made similar researches on the *Succiso- Molinietum hungaricae* stands of the same meadows. Németh (2000) made the vegetation map of the enlargement of the Ásotthalmi Láprét, Papp (2000) made it for the marsh meadow called Halászka.

The marsh meadow of Zákányszék is one of the depressions between the sand dunes of Kiskunság that were formed by the most frequent NW direction wind and have an orientation in a NW-SE direction. It is characterized by heterogeneous microrelief conditions; it contains sand dunes, wet depressions and the transitional levels between them.

Consequently the vegetation is diverse and mosaic-like, it is partly composed of transitional stands that cannot be identified with vegetation types written in the literature (Borhidi and Sánta 1999, Fekete *et al.* 1997). Recent anthropogenic impacts (drying out as a result of the canalization and grazing) could have played an important role in the formation of these stands.

The nature of transitional stands is one of the main topics of the coenology of today (Bagi 1998, Körmöczi *et al.* 2002, Zalatnai and Körmöczi 2002); it gives the actuality of my researches. The investigation of the marsh meadow of Zákányszék is a part of the research that was aimed by Margóczi *et al.* (1998) and it is important also from the point of view of nature conservation. It can contribute to the protection of its valuable vegetation. It is a value also as a wetland with its flora and fauna. Its value is also increased by the sand-steppe meadow that can be found only in small patches today and is threatened by disappearing.

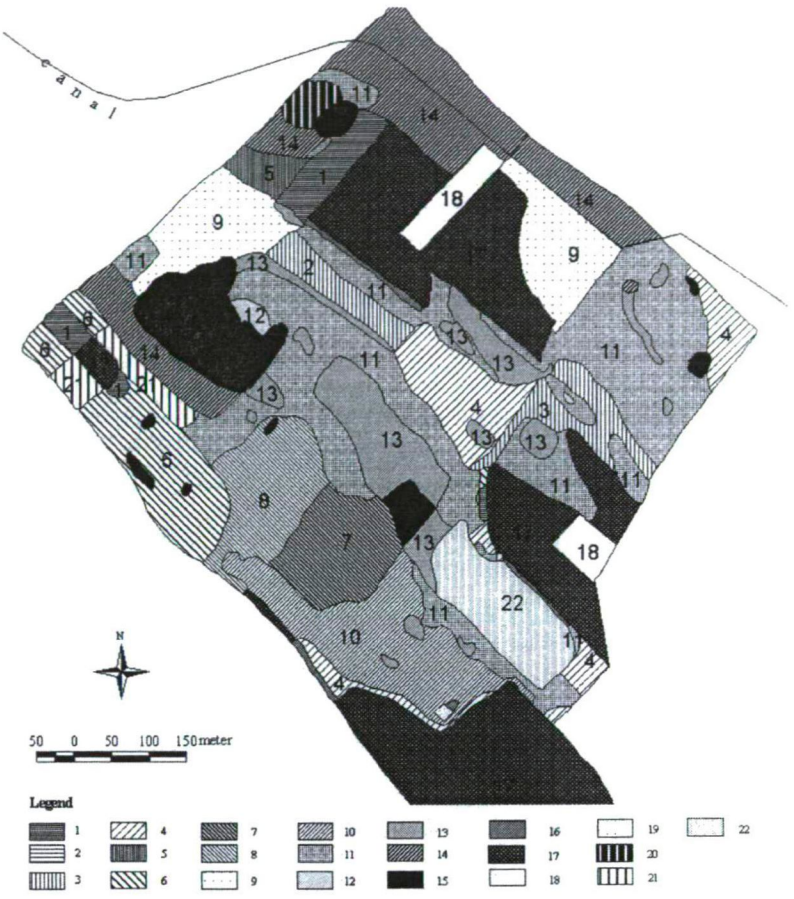

Fig. 1. The vegetation map of the marsh-meadow of Zákányszék (2001)
1: *Rhinanthus* type of *Astragalo austriacae-Festucetum sulcatae*, 2: *Genista* type of *Astragalo austriacae-Festucetum sulcatae*, 3: *Anacamptis* type of *Astragalo austriacae-Festucetum sulcatae*, 4: *Dactylis* type of *Astragalo austriacae-Festucetum sulcatae*, 5: transitional unit between *Astragalo austriacae-Festucetum sulcatae* and *Succiso-Molinietum hungaricae*, 6: transitional unit between *Agrostio-Caricetum distantis* and *Astragalo austriacae-Festucetum sulcatae*, 7: *Festuca pratensis* type of transitional unit between *Agrostio-Caricetum distantis* and *Astragalo austriacae-Festucetum sulcatae*, 8: transitional unit between *Agrostio-Caricetum distantis* and *Succiso-Molinietum hungaricae*, 9: *Succiso-Molinietum hungaricae*, 10: *Carex flacca* type of *Succiso-Molinietum hungaricae*, 11: *Agrostio-Caricetum distantis*, 12: *Lepidio crassifolii-Puccinellietum limosae*, 13: salt-affected marshes (*Schoenoplectetum tabernaemontani* and *Bolboschoenetum maritimi*), 14: large sedge communities (*Caricetum acutiformis* and *Caricetum ripariae*), 15: dry reed beds (*Phragmitetum communis* and *Bolboschoeno–Phragmitetum*), 16: weed vegetation, 17: ploughland, 18: farm, 19: pit for loam-mining, 20: mosaic of *Succiso-Molinietum hungaricae* and salt-affected marshes, 21: mosaic of large sedge communities and *Agrostio-Caricetum distantis*, 22: mosaic of dry reed beds and salt-affected marshes

Methods

The marsh meadow of Zákányszék is in the southern Kiskunság, in the geographical area called Dorozsma–Majsai–sand plateau, in the outskirts of Zákányszék. It belongs to the floristic region of the Eupannonicum (Great Plain), within it to the flora district of them Praematricum (Duna–Tisza köze). It's area is 115 ha and the mapped part is 56 ha.

According to Urbán (1999), the soil of the investigated steppe meadow stands within the marsh meadow of Zákányszék is slightly heavy, the upper layer is loam-sandy loam, below rather sand, coarse sand. The soil is slightly salt-affected, the sodium content is low.

The soil of the marsh analysed by Urbán (1999) is heavy, the heaviness figures are the highest in the upper layer and gradually going deeper the water retention and the loam content of the soil decreases (Madarász 2000). Its humus content is high.

The vegetation map (Fig. 1) was made on the basis of EOTR map (1978) on scale 1:10000 and a black and white aerial photograph (1989) on scale 1:10000 (Seregélyes and Csomós 1995). The scale of the map is 1:5000. It was elaborated in 2001. In the paper the denomination of vegetation units is in accordace with the literature (Borhidi and Sánta 1999) if it is possible but I did not categorized the transitional units and the units below the association level. On a small part of the area we fixed points using teodolite for making a test; the points fitted to the map created by spacing with an error of maximum 5 m.

In order to make objective sampling I made coenological quadrats of 5×5 m that were placed on homogenous sites representing vegetation types distinguished by the field experience. 44 relevés were made in May and June in 2000. I made classification and principal components analysis (PCA) based on correlation matrices. In the classification process the Ward-method was used as fusion algorithm. This method combines groups well at low difference level but the increasing of the hierarchical levels doesn't carry information about the structure of data. The Manhattan-metrics („city block"-metrics) was used as comparative function (Podani 1997).

The average of possibly relevant ecological indicator values weighted with the cover of species as variables were calculated for every plot. These indicator values are the followings: the indicator values of the relative groundwater and soil moisture (WB), the relative values of the nitrogen demand (NB), the relative values of the soil reaction (pH) (RB) and the average scale values for signing the halophyte and halophilous plants (SB) (Borhidi 1993). I calculated correlation between the PCA coordinates of plots and their average indicator values (indirect gradient analysis, Podani 1997) using a non-parametric test, the Spearman rank correlation (Barta *et al.* 2000). Because of using more than one rank correlation with the given variables in order to decrease the first order deviation. I made Bonferroni correction: I divided the $\alpha = 0.05$ significance level by the number of tests (12). The new significance level was $\alpha = 0.00417$. I correlated the ecological indicator values with each other using the same method. The significance level after the Bonferroni correction was $\alpha = 0.00625$.

I carried out the statistical analysis using the STATISTICA for Windows 5.0 (StatSoft Inc. 1984-1995) software.

Results and Discussion

Vegetation units

Based on the field experiences I distinguished the vegetation units as follows:

Astragalo austriacae-Festucetum sulcatae Soó 1957 (AF),

Succiso-Molinietum hungaricae (Komlódi 1958) Soó 1969 (SM),

Agrostio-Caricetum distantis (Rapaics ex Soó 1938) (AC),

Scorzonero parviflorae-Juncetum gerardii (Wenzl 1934) Wendelberger 1933,

Lepidio crassifolii-Puccinellietum limosae Soó (1947) 1957,

salt-affected marshes (*Schoenoplectetum tabernae-montani* Soó 1947 and *Bolboschoenetum maritimi* Eggler 1933),

Caricetum acutiformis Eggler 1933 and *Caricetum ripariae* Soó 1928 (CA),

Phragmitetum communis Soó 1927 em. Schmale 1939,

Bolboschoeno–Phragmitetum Borhidi et Balogh 1970,

transitional unit between *Agrostio-Caricetum distantis* and *Astragalo austriacae-Festucetum sulcatae* (AC-AF),

transitional unit between *Astragalo austriacae-Festucetum sulcatae* and *Succiso-Molinietum hungaricae* (AF-SM),

transitional unit between *Agrostio-Caricetum distantis* and *Succiso-Molinietum hungaricae* (AC-SM).

Astragalo austriacae-Festucetum sulcatae (AF)

The highest relieves of the sand dunes are covered by plough-lands. Around them the sand-steppe meadow (AF) association is characteristic. Its coverage is about 90 %. The dominant species are *Festuca rupicola* and *Festuca pseudovina* in the lower, thick level, *Chrysopogon gryllus, Dactylis glomerata* and *Festuca pratensis* in the upper level (Table 1).

The present sand-steppe meadows can be classified as so called 'lake steppes', formed from *Succiso-Molinietum hungaricae* association by dehydration and is characterized by the dominant and constant species *Chrysopogon gryllus* within AF. They were congruent also with the description of the sand-steppe meadows formed from SM by drying out (Molnár and Varga 1997, Rédei 1999). The present species of tall herb humid meadows and hay meadows (*Genista tinctoria, Orchis coriophora, Polygala comosa, Poa pratensis, Ranunculus acris,*

Table 1. Relevés of AF with the coverage percents of plant species.

number of relevés	2	4	5	7	10	11	14	19	30
Achillea asplenifolia	0.1		1	0.1		0.1		30	2
Achillea pannonica		0.1	8	0.1	0.1				
Agropyron repens		5	0.1	0.1				3	15
Anacamptis pyramidalis					1	0.5			
Centaurea sadlariana	0.1				2	1			
Chrysopogon gryllus	0.1	15		2	30	10			4
Coronilla varia	5	5	0.1	30	5	4			1
Cynodon dactylon	2			0.1					
Dactylis glomerata	20	30	40	15	30	30	40	5	25
Festuca pratensis	10		15	15			10	30	30
Festuca pseudovina	0.1		5						
Festuca rupicola						10	8	15	30
Filipendula vulgaris						8			
Galium verum		3	0.1				2	3	3
Genista tinctoria		12	8					0.1	
Holoschoenus romanus		0.1		2	1	3			1
Hypochoeris maculatum	0.1	0.1			20	8			
Knautia arvensis	1				0.1	0.1			
Koeleria cristata	15	1	0.1			5			
Linum perenne	5	0.1		3	0.1	0.1	10	0.1	0.1
Lotus corniculatus	0.1	0.1				4		1	0.1
Ononis spinosa	10	5		5	5	4	3	3	3
Plantago lanceolata	3	5			1	0.1			0.1
Poa angustifolia		0.1		0.1		5		5	2
Polygala comosa	10	0.1				0.1			
Rhinantus minor	10	0.1	8	10		0.1		0.1	0.1
Salvia pratensis		10		10	3	3			
Silene vulgaris	0.1	0.1	0.1	0.1	0.1		1	0.1	
Taraxacum officinalis	1		0.1	1	0.1	0.1			

Species with a coverage of 0.1 % in one or more relevés: *Anthyllis vulneraria, Arenaria serpillifolia, Bromus arvensis, Bromus mollis, Campanula sibirica, Carex cariophyllea, Carex distans, Carex flacca, Centaurea pannonica, Dianthus pontederae, Lathyrus silvestris, Medicago falcata, Medicago lupulina, Molinia arundinacea, Muscari botryoides, Ophrys sphecodes, Orchis coriophora, Ornithogalum umbellatum, Pastinaca sativa, Plantago maritima, Poa pratensis, Podospermum canum, Ranunculus acris, Rumex acetosa, Verbascum phoeniceum, Vicia angustifolia.*

Ophrys sphecodes) also refer to marsh origin. Most of the other characteristic species were absent, such as the *Astragalus austriaca* that is included in the name of the association.

The subunits of this unit are *Linum-Rhinanthus, Genista tinctoria, Anacamptis* and *Datylis-Festuca* pratensis types according to physiognomy and species combination. From these types the *Anacamptis* type fits most the description of AF association. It is similar to the *Salvia-Filipendula* type of the AF association described by Papp (2000) from Halászka, as well as to the *Centaurea* type of steppe grassland. The speciality of this subunit is the joint presence of *Ophrys sphecodes, Orchis coriophora* and *Anacamptis pyramidalis*, that has not been observed in other grasses in the southern Kiskunság. The *Dactylis-Festuca pratensis* type is degraded, the high dominance of monocotyledons (*Dactylis glomerata* and *Festuca pratensis*, mostly) and the taller vegetation distinguish this type from others. Its stands are mowed regularly, the high dominance of *Festuca pratensis* and *Dactylis glomerata* can be the result of sowing.

Succiso-Molinietum hungaricae (SM)

On a bit deeper relief patches of calcareous purple moorgrass meadow (SM) develop (Table 2). Most of them are not typical SM stands. The *Deschampsia* type of SM corresponds to the descriptions in the literature. The *Carex flacca* type of SM association corresponds to the *Molinietum serratuletosum tinctoriae* subassociation, the driest one described by Bodrogközy (1961).

The typical SM stands can be characterized by the high dominance of *Molinia hungarica.*

The *Carex flacca* type of SM association has a coverage of 90-100 %. Its dominant and characteristic species are the *Molinia hungarica* and *Carex flacca.*

Table 2. Relevés of SM with the coverage percents of plant species.

number of relevés	8	26	28	29	32	33	35	37	45
Achillea asplenifolia				1	2	1	1		0.1
Agropyron repens	0.1						15		
Agrostis alba	5		2						
Bromus arvensis							3		
Carex distans	0.1	5		2	2		4		
Carex flacca			30	60	70	70	20	60	
Carex panicea	0.1	5	30	20	1		2	10	
Carex tomentosa	5						1		
Carex vulpina		5					5	2	
Centaurea pannonica	0.1	0.1	0.1	0.1	1	1	0.1	0.1	0.1
Deschampsia caespitosa	40	40					40		
Festuca pratensis	30						2		
Festuca pseudovina					10				
Festuca pseudovina and F. rupicola						10			
Festuca rupicola									10
Festuca sp. (pseudovina or rupicola)				40					
Galium verum			0.1	1	2	1			0.1
Holoschoenus romanus			0.1	2		3	5		
Juncus articulatus	3	1	1				1		
Juncus compressus	3							1	
Koeleria cristata								15	
Molinia arundinacea						5			
Molinia hungarica				0.1			0.1		75
Ononis spinosa		1		3	1	2	0.1		
Poa angustifolia								2	
Ranunculus acris	2	5			0.1	0.1	0.1	0.1	
Sanguisorba officinalis	0.1		6	5	4	2	2		
Serratula tinctoria			2	5	1	1	0.1	3	1

Other species in the relevés: *Carex hirta, Cynodon dactylon, Dactylis glomerata, Linum perenne, Lotus siliquosus, Lysimachia vulgaris, Orchis laxiflora ssp. Palustris, Phragmites australis, Plantago lanceolata, Plantago major, Plantago maritima, Potentilla anserina, Potentilla reptans, Silene multiflorum, Taraxacum officinalis, Thalictrum flavum, Trifolium pratense, Triglochin maritima.*

The *Succiso-Molinietum hungaricae deschampsietum* subassociation can be distinguished obviously based on the high coverage of *Deschampsia caespitosa* that is a characteristic species of tall herb humid meadows and hay meadows (Simon 1999) and its presence here refers to degradation. The characteristic species of AC are also present but only with much lower coverage than in AC-SM.

Agrostio-Caricetum distantis (AC)

In similar relief AC covers large areas where low water coverage is present in spring. Within the stands the *Carex distans* and *Agrostis stolonifera* dominate in varying proportion, therefore the vegetation is patchy (Table 3). The joint coverage of this two species is about 50-70%, the total coverage is 60-80 %. It is poor in species which can refer to secondary formation as according to Molnár (1997) a big part of AC stands were formed from marshes secondarily (with the getting of vegetation zones in deeper relieves after water management works) and this has resulted the decreased species richness. There are species characteristic or frequent in salt-affected associations. The presence of *Festuca pseudovina, Festuca arundinacea, Plantago maritima, Linum perenne, Potentilla reptans, Poa angustifolia* and *Cynodon dactylon* refers to degradation or drying out (Molnár in Fekete *et al.* 1997). *Schoenoplectetum tabernae-montani* patches can be found in some of its dips. In deeper relieves *Agrostis stolonifera* dominates rather than *Carex distans* and *Bolboschoenus maritimus* can be dominant as well. These stands are closer to the *Agrostidetum stoloniferae* Soó (1940) 1968 association but I have not separated them on the map because of their small extent. They are poorer in species than the AC stands and *Cirsium brachycephalum* appears beside *Bolboschoenus maritimus*. In deeper relief this unit is substituted by *Lepidio crassifolii-Puccinellietum limosae* association. In the wettest parts *Eleocharis palustris* appears and becomes dominant. The types of AC above (types dominated by *Eleocharis palustris* and by *Agrostis stolonifera* and typical *Agrostio-Caricetum distantis*) and the *Festuca pratensis* type of the transitional unit between AC and AF can

correspond to the *Eleocharis palustris→ Agrostis alba→ Carex distans-Plantago maritima→ Festuca arundinacea-Carex distans* series (Rapaics 1927).

Table 3. Relevés of AC with the coverage percents of plant species.

number of relevés	13	18	31	34
Achillea asplenifolia			0.1	
Agrostis alba	10	40	30	70
Calystegia sepium		0.1		
Carex distans	50	10	20	1
Carex panicea				0.1
Eleocharis palustris				0.1
Euphorbia palustris	0.1			
Festuca arundinacea	5			
Festuca pratensis		2		
Festuca sp. (F. pseudovina or *F. rupicola)*			15	
Holoschoenus romanus			4	
Juncus articulatus				0.1
Juncus compressus	1			3
Juncus gerardii			0.1	
Lotus corniculatus			0.1	
Molinia arundinacea			1	
Orchis laxiflora ssp. palustris		0.1	0.1	
Plantago lanceolata		0.1		
Plantago maritima			0.1	
Potentilla anserina				0.1
Potentilla reptans				2
Sanguisorba officinalis			0.1	
Serratula tinctoria	0.1	0.1	0.1	
Thalictrum flavum		0.1		

Transitional unit between Agrostio-Caricetum distantis and Astragalo austriacae-Festucetum sulcatae (AC-AF)

The AC-AF can be found in similar relief. Species of the AC and the AF associations and in patches of the SM are mixed in them (Table 4). The high dominance of *Carex distans* is characteristic. It shows similarity with the *Potentillo-Festucetum pseudovinae* typicum *caricosum distantis* subassociation described by Bodrogközy (1961) but it is not equal with it. The *Festuca pratensis* type of this unit is marked on the vegetation map. It can be characterized by high dominance of the *Festuca pratensis* and as a result the different phisiognomy (taller and denser grass).

Transitional stand between Astragalo austriacae-Festucetum sulcatae and Succiso-Molinietum hungaricae (AF-SM)

An AF-SM stand can be found next to one of the AF stands, in a bit deeper relief. It is dense and mosaic-like. The mosaic is created by patches dominated by *Festucion* and *Molinion* species (Table 5). Based on its species composition it is closer to the *Linum-Rhinanthus* type of sand-steppe meadow, but *Molinia hungarica* appears and the *Molinion* species have higher coverage. The largest population of *Ophrys sphecodes* can be found here, partly spread across to the neighbouring AF (*Linum-Rhinanthus* type) stand. It can be observed that from the SM towards the AF the *Orchis laxiflora* subsp. *palustris*, the *Ophrys sphecodes* and the *Orchis coriophora* appear by turns (Molnár and Varga 1999).

Table 4. Relevés of AC-AF with the coverage percents of plant species.

number of relevés	6	17	20	24	25	36	38
Achillea asplenifolia	5	0.1	20	10	3	10	4
Agrostis alba			5				
Carex cariophyllea		8					
Carex distans	40	30	30	25	60	40	12
Chrysopogon gryllus	10	12	3	2			20
Coronilla varia		2					
Cynodon dactylon	0.1				1	10	
Dactylis glomerata		3	1			1	8
Festuca pratensis	10	2	10	5	5	10	20
Festuca pseudovina	6				10		
Festuca rupicola		12	10			10	8
Festuca sp. (F. pseudovina or F. rupicola)				8			
Galium verum		0.1	0.1	0.1	0.1	4	3
Koeleria cristata						3	5
Linum perenne	8	1	0.1	3	2	3	
Lotus corniculatus	0.1	2	0.1	0.1	0.1	0.1	
Molinia hungarica	2			2			
Ononis spinosa	0.1	1	2	2		1	3
Plantago lanceolata		8	0.1				0.1
Rhinantus minor	5	5	1	0.1		0.1	4
Serratula tinctoria		0.1		5		0.1	

Other species in the relevés: *Achillea pannonica, Bromus arvensis, Campanula sibirica, Carex panicea, Centaurea pannonica, Centaurium erythraea, Euphrasia tatarica, Knautia arvensis, Linum catarticum, Lotus siliquosus, Molinia arundinacea, Orchis coriophora, Plantago maritima, Podospermum canum, Polygala comosa, Puccinellia limosa, Scorzonera parviflora, Taraxacum officinalis.*

Transitional unit between Agrostio-Caricetum distantis and Succiso-Molinietum hungaricae (AC-SM)

The stand of AC-SM is denser than the AC stands. Some species of marshes occur in it but the dominant species is Carex distans so considering the species composition it is closer to the AC association (Table 6). The other characteristic species of the AC association, Agrostis stolonifera occurs only with low coverage. This unit can be equal with the salt-affected meadow with Molinia (Bodrogközy, 1961), it is close to the Serratula tinctoria facies of this unit.

Table 5. Relevés of AF-SM with the coverage percents of plant species.

number of relevés	3	27
Achillea asplenifolia	1	
Carex cariophyllea	10	
Carex flacca	10	40
Centaurea sadlariana	0.1	2
Chrysopogon gryllus	30	0.1
Cynodon dactylon	5	
Dactylis glomerata	3	8
Festuca pratensis	0.1	10
Galium verum	0.1	1
Holoschoenus romanus	3	0.1
Linum perenne	2	
Lotus corniculatus	3	0.1
Molinia arundinacea		5
Ononis spinosa	10	5
Orchis coriophora	0.5	
Salvia pratensis	10	0.1

Species with a coverage of 0.1 % in one or more relevés: *Achillea pannonica, Agropyron repens, Agrostis alba, Carex panicea, Dianthus pontederae, Euphrasia tatarica, Festuca sp., Genista tinctoria, Juncus gerardii, Linum catarticum, Lotus siliquosus, Muscari botryoides, Ornithogalum umbellatum, Plantago lanceolata, Polygala comosa, Ranunculus acris, Rhinantus minor, Rumex acetosa, Silene vulgaris, Taraxacum officinalis, Thalictrum lucidum.*

Table 6. Relevés of AC-SM with the coverage percents of plant species.

number of relevés	9	15	23	39	44
Agrostis alba		15	5	30	
Carex distans	30	30	30	10	60
Festuca pratensis	0.1		1	20	
Festuca pseudovina	1		1		
Festuca rupicola				20	
Galium verum			0.1		2
Holoschoenus romanus	10				4
Molinia arundinacea	40				
Molinia arundinacea and *M. hungarica*		15			
Molinia hungarica			30	15	15
Ononis spinosa	8		0.1		4
Sanguisorba officinalis	2	5		5	
Serratula tinctoria	5	5	3	3	1
Triglochin maritimum				2	

Other species in the relevés: *Achillea asplenifolia Agropyron repens Carex panicea Centaurea pannonica Cynodon dactylon Euphorbia palustris Genista tinctoria Iris pseudacorus Juncus gerardii Linum perenne Lotus corniculatus Lotus siliquosus Orchis laxiflora ssp. palustris Plantago maritima Podospermum canum Ranunculus acris Silene vulgaris Taraxacum officinalis.*

Scorzonero parviflorae-Juncetum gerardii

The *Scorzonero parviflorae-Juncetum gerardii* (Wenzl 1934) Wendelberger 1933 association occurs in small patches inserted in large sedge communities and AC stands. I haven't draw these patches on the map because of their small extend. The high dominance of *Juncus gerardii* is characteristic. Other frequent species: *Festuca arundinacea, Orchis laxiflora* subsp. *palustris, Serratula tinctoria* and *Euphorbia palustris.*

Lepidio crassifolii- Puccinellietum limosae

The *Lepidio crassifolii-Puccinellietum limosae* Soó (1947) 1957 stands are poor in species and have low coverage. Characteristic species: *Puccinellia limosa, Lepidium crassifolium, Aster tripolium subsp. pannonicus.*

Salt-affected marshes

In the deepest relieves, in natural depressions with water coverage in spring and in pits used for loam-mining salt-affected marshes (*Schoenoplectetum tabernaemontani* Soó 1947 and *Bolboschoenetum maritimi* Eggler 1933) covers large areas. Its stands are poor in species, the dominant species cover almost the whole area (Table 7). Total coverage is 45-70 %. The alternating of dominant species makes the vegetation mosaic-like (see Bagi 1999a, b, 1997).

Table 7. Relevés of salt-affected marshes with the coverage percents of plant species.

number of relevés	12	22	41	42	43
Agrostis alba		10			
Bolboschoenus maritimus	15	20	15	35	
Calystegia sepium			0.1	0.1	0.1
Carex distans		0.1			
Eleocharis palustris	15	20	25	4	20
Euphorbia palustris					0.1
Galium palustre					0.1
Juncus gerardii		0.1			0.1
Lysimachia vulgaris			0.1		
Lythrum salicaria					0.1
Phragmites australis					2
Schoenoplectus tabernae-montani	15	1	25	10	30
Thalictrum flavum					0.1
Triglochin maritimum			1	0.1	

Different types of salt-affected marshes according to the dominant species are the following:

Schoenoplectus tabernae-montani type that is equal with the *Schoenoplectetum tabernaemontani* (Soó 1947) association,

Bolboschoenus maritimus type that is equal to the *Bolboschoenetum maritimi* (Eggler 1933) association,

Schoenoplectus tabernaemontani-Bolboschoenus maritimus type – the species of the two associations are frequently mixed also according to Bagi (1999a,b),

Bolboschoenus maritimus-Eleocharis palustris type that is equal to the *Bolboschoenetum maritimi* (Eggler 1933) association with the codominant species of *Eleocharis palustris*,

Bolboschoenus maritimus-Agrostis stolonifera type,

Bolboschoenus maritimus-Agrostis stolonifera-Eleocharis palustris type,

Bolboschoenus maritimus-Juncus gerardii type that is equal with the *Bolboschoenetum maritimi* (Eggler 1933) association but *Juncus gerardii* became codominant.

The *Schoenoplectetum tabernaemontani* Soó 1947 and the *Bolboschoenetum maritimi* Eggler 1933 associations are not isolated on the map, because they create a mosaic with each other on a smaller scale. The stands cannot be grouped in the subassociations described by Bodrogközy (1961).

Table 8. Relevés of large sedge communities with the coverage percents of plant species.

number of relevés	1	16	21	40
Agrostis alba	10	15		12
Caltha palustris	4		8	
Carex acutiformis			50	
Carex distans		2		10
Carex panicea	0.1	2		0.1
Carex riparia	20	30		30
Carex vulpina			2	
Deschampsia caespitosa	10			
Equisetum palustre	20			
Euphorbia palustris	0.1	0.1		7
Festuca pratensis				5
Festuca rupicola				10
Holoschoenus romanus		4		2
Juncus articulatus	10		0.1	
Juncus compressus	10			
Lysimachia vulgaris	2		8	
Mentha aquatica	1			
Molinia arundinacea		10		
Ranunculus acris	0.1	0.1	5	0.1
Sanguisorba officinalis	0.1	8	15	6
Serratula tinctoria		8		3
Thalictrum flavum	1	0.1		0.1

Species that occur in some relevés with 0.1 % coverage: *Calystegia sepium, Centaurea pannonica, Galium palustre, Galium verum, Iris pseudacorus, Juncus gerardii, Lotus corniculatus, Orchis laxiflora ssp. Palustris, Poa angustifolia, Poa pratensis, Thalictrum lucidum, Vicia cracca.*

Large sedge communities

The large sedge communities (*Caricetum acutiformis* Eggler 1933, *Caricetum ripariae* Soó 1928) also cover large areas in deep relieves. Its stands are dense, the height is about 100 cm. The dominant sedge species are *Carex riparia* and *Carex acutiformis* (Table 8). The stands can be grouped in the *Caricetum acutiformis-ripariae eleocharetosum palustris* (Soó 1927) subassociation. The stand next to a reed stand is a transition towards *Agrostio-Caricetum distantis* association. This transitional stand differs from both units considering its physiognomy. *Carex distans* and *Carex acutiformis* mix in it with equal coverage.

Dry reed beds

In the deepest relieves dry reed beds (*Phragmitetum communis* Soó 1927 em. Schmale 1939 and *Bolboschoeno–Phragmitetum* Borhidi et Balogh 1970) cover some smaller and larger patches. The two reed associations are not separated from each other sharply, usually the *Phragmitetum communis* is characteristic in the centre of the reed stands, and the *Bolboschoeno–Phragmitetum* at the edges. They form clumps in patches, on the clumps *Agrostis stolonifera, Lythrum salicaria* and *Calystegia sepium* have settled. Other frequent species: *Mentha aquatica, Utricularia vulgaris, Galium palustre, Lythrum salicaria, Equisetum palustre, Caltha palustris.* Gradual transition can be observed from the *Agrostio-Caricetum distantis* towards the *Bolboschoeno–Phragmitetum.*

Protected plant species

We have found one strictly protected plant species and nine protected species in the area (Table 9).

The relationships between vegetation units

The described three transitional units are not in transitional stripes but create separate, extended stands. They are probably temporal transitions. Their patchiness can be the result of abiotic heterogeneity (Bagi 1998). The formation of the temporal transitions can mainly be the result of the drying out, the changing of the water table level and with this the level of salinity. The joint presence of certain species of the different vegetation units shows that the characteristic species of certain associations can colonize in other associations. If the drying out of the area continues it can be expected that the AF-SM stand would turn into AF association.

As a result of the cluster analysis (Fig. 2) the coenological samples of the *Bolboschoenetum maritimi*, the *Deschampsia* type of SM, *Carex flacca* type of SM and the AF were grouped obviously in separate clusters. There are separate clusters of the relevés of large sedge communities, AC, and from the transitional units the two transitions of the AC but some samples of them got to other groups. A mixed cluster has also formed. It includes the plots of the latter units which indicates that there are not

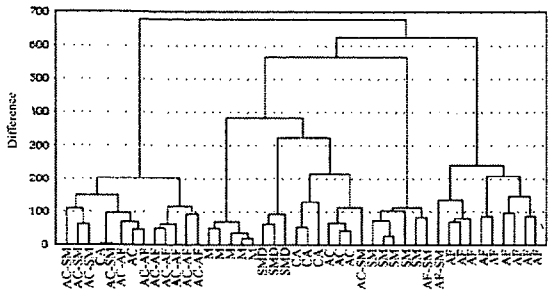

Fig. 2. The result of cluster analysis of 44 coenological relevés. The abbreviations mean: AC-SM: transitional unit between *Agrostio-Caricetum distantis* and *Succiso-Molinietum hungaricae*, CA: large sedge communities (*Caricetum acutiformis* and *Caricetum ripariae*), AC-AF: transitional unit between *Agrostio-Caricetum distantis* and *Astragalo austriacae-Festucetum sulcatae*, M: salt-affected marshes (*Schoenoplectetum tabernaemontani* and *Bolboschoenetum maritimi*), SMD: *Succiso-Molinietum hungaricae deschampsieostum*, AC: *Agrostio-Caricetum distantis*, SM: *Succiso-Molinietum hungaricae Carex flacca* type, AF-SM: transitional unit between *Astragalo austriacae-Festucetum sulcatae* and *Succiso-Molinietum hungaricae*, AF: *Astragalo austriacae-Festucetum sulcatae*.

sharp differences between them. One of the samples of the AF-SM got into the cluster of the *Carex flacca* type of SM, the other into the cluster of the AF so this method did not confirm the independence of this transitional unit. The cause of it can be that this unit is mosaic-like, the different patches within the stands are distinguished by the dominance of the species of the two 'clear' unit, and the relevés were made in these patches. The cluster analysis has confirmed the independence of all the vegetation units that were distinguished by the field experience also the transitional units except the AF-SM.

As a result of the principal component analysis (Fig. 3) the relevés of the AF, the AF-SM, the two types of SM, the salt-affected marshes and the AC-AF were placed in separate clouds of points. Sample nr. 38 was made in an AF stand with *Carex distans* that's why it is separated from the group of AF relevés. The samples of the large sedge communities, and especially the AC and the AC-SM are segregated from each other more or less along the first axis, and are drawn apart along the second axis. This emphasizes the spatially variable rate of the marsh species in the case of the AC-SM. In the case of the AC the drawing apart can be related with the gradual changing of the proportion of the two dominant species. The patchiness resulted in the spatially (on scale of sampling) alternating dominance of the two dominant species is characteristic in AC stands, the used method emphasizes this. The samples of the AF-SM are between the relevés of AF and SM along the second axis. The relevés of the AC-AF are placed between the plots of the AC and the AF along the second axis and they are close to some of the relevés of the AC. The relevés of the AC-SM are close to the relevés of the AC along the first axes and to the SM along the second axis. The variance proportion for the first three components of the PCA is low (49.12914%) because of the large number of the

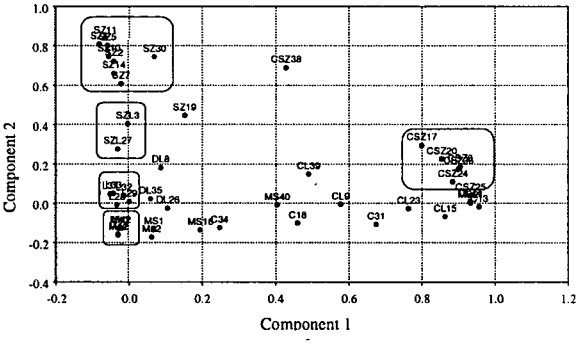

Fig. 3. The result of the principal component analysis of 44 relevés. The abbreviations mean: CL: transitional unit between *Agrostio-Caricetum distantis* and *Succiso-Molinietum hungaricae*, MS: large sedge communities (*Caricetum acutiformis* and *Caricetum ripariae*), CSZ: transitional unit between *Agrostio-Caricetum distantis* and *Astragalo austriacae-Festucetum sulcatae*, M-salt-affected marshes (*Schoenoplectetum tabernaemontani* and *Bolboschoenetum maritimi*), DL: Succiso-*Molinietum hungaricae deschampsietum*, C: *Agrostio-Caricetum distantis*, L: *Succiso-Molinietum hungaricae* Carex flacca type, SZL: transitional unit between *Astragalo austriacae-Festucetum sulcatae* and *Succiso-Molinietum hungaricae*, SZ: *Astragalo austriacae-Festucetum sulcatae*.

variables. For increasing this we made PCA separately for groups of vegetation units of which relationships are specially interesting – the transitions and the adequate 'clear' units. The coenological samples were placed in a similar way as in the case of the joint ordination, consequently the lower variance proportion explains well the relations of the coenological plots.As a result of the indirect gradient analysis the first component correlates with SB (R=0.699, p=0,0000001, N=44), the second component with WB (R= -0.846, p= 0.0000000, N=44) and with SB (R=-0.502, p=0.0005096, N=44). The third component shows correlation with NB (R=-0.502, p= 0.0005096, N= 44). WB correlates with SB. This result confirm that it is expectable that the soil moisture conditions controlled by the depth of the soil water table and the level of salinity plays a considerable role in the formation of the spatial pattern of the vegetation as in case of other grasses

Table 9. The protected plant species of the area.

Species	Population size (in 2000)	Habitat description
Ophrys sphegodes	578, 100, 200 (in 1999)	contact zone of calcareous purple moorgrass meadow and sand-steppe meadow; *Genista* and *Anacamptis* types of sand-steppe meadow
Anacamptis pyramidalis	800-1000	*Anacamptis* type of sand-steppe meadow
Blackstonia acuminata	5	in a pit covered by *Agrostio-Caricetum distantis* stand
Centaurea sadleriana	of order of 10000	
Dianthus superbus	1500	large sedge community
Iris sibirica	120	pits and patches of calcareous purple moorgrass meadow sporadically
Iris spuria	25	a pit covered by *Bolboschoenetum maritimi*
Muscari botryoides	105, 235, 2, 27000 (estimation), and 13500 (estimation) (in 1999), altogether 3000 stems (in 2000)	sand-steppe meadow
Orchis laxiflora subsp. *palustris*	of order of 10000	present in the whole area except the sand-steppe meadows
Orchis coriophora	350 and 250	sand-steppe meadow; transitional stand of sand-steppe meadow and calcareous purple moorgrass meadow

(for example see Mile *et al.*, 2001). Salt-affected vegetation units occur only in the depressions with temporary water coverage, halophyte species are not present in drier units or only with very low coverage. This explains the correlation between average values of WB and SB.

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TISCIA 34, 15-18

BIOLOGICAL CONTROL OF MOSQUITOES BY AQUATIC PLANARIA

Suprakash Kar and A. K. Aditya

Suprakash Kar and A. K. Aditya (2003): Biological control of mosquitoes by aquatic planaria. — *Tiscia 34, 15-18.*

Abstract. This paper presents an idea of biological control of mosquitoes by their predators, the planarians. The suggested technique for biological control would be of special interest, because unlike pesticides, it does not cause secondary environmental effects as pollutant. The aim of the paper is to demonstrate the potential application of planarians as predators of the mosquitoes at their developmental stage.

Key words: environment, mosquito, planaria, prey-predator

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Introduction

In India, the status of mosquitoes, as the carrier of different parasites and acting as secondary host of different diseases is a menace to human existence. They are indirectly fostered by the inexorable condition of the society to grow, increase number and some times even to the extent of causing baneful effect. This is necessarily due to the ignorance of the life cycle of mosquitoes by the common men. Oils and insoluble surfactants such as Arosurf 'Monomolecular Surface Film', insect juvenile hormone analogues such as methoprene, and natural enemies can be introduced as biological control agents (Laird and Miles 1985) against the aquatic stages of mosquitoes. Certain pesticides and chemicals can significantly and effectively control the population of mosquitoes. The chemicals, however, pollute the entire water of the breeding areas, causing additional environmental problems.

These harmful chemicals can no doubt destroy the mosquitoes but at the same time directly/indirectly being accumulated in the different members of the food chain and get magnified causing damage to the members of higher tropic level. The 'biological control' becomes very effective measure to avoid such hazards. Microbial control agents including bacteria such as *Bacillus thuringiensis israelensis*, which is commercially available for application to mosquito larval habitats and the fungi *Coelomomyces* and *Culicinomyces* (Meritt *et al.* 1992, Clements 1992) are also in practice for such purpose. Parasitic nematodes have also been suggested for biological control of mosquito larvae. The dragonfly larvae (Sebastian *et al.* 1990), the water boatman *Notonecta* (Guthrie 1989), the magnificent predatory mosquito *Toxorhynchites*, and fishes such as the mosquito fish *Gambusia affinis* or the guppy *Poecilia reticulata* (Cutris 1991) are some of the potentially useful predators for control of the mosquitoes.

The purpose of the present work is to demonstrate as to demonstrate how the larvae of the mosquitoes can be destroyed by planarians, *Dugesia bengalensis* which feed on them. A suitable technique for biologically controlling the development as well as checking the population of mosquitoes has been adopted by producing large number of its predators. In this context, planarians, the free-living helminthes play a very important role. These organisms can be cultured very easily in the stagnant water with other microorganisms (Kawakatsu *et al.* 1983, Aditya *et al.* 1989, 1991) and also in ponds and lakes. They breed by both asexual (by binary fission, Aditya *et al.* 1987) and sexual processes and these organisms are carnivorous in habit (Kawakatsu *et al.* 1975) and can tolerate a temperature range up to 32°C.

Materials and Methods

The culture of the mosquitoes (both *Anopheles* and *Culex*) and their predators (Planarian: *Dugesia bengalensis*) is being maintained in the laboratory separately. The cement cisterns and some large containers with wide-open mouth are used for this purpose.

The planarians being maintained in small tanks (1.5′ × 1′ × 1.5′) / enamel trays (1′ × 6″ × 1.5″) and with proper and careful handling and with food supplement might yield to considerably increased number within short time. The planarians are usually supplied with fresh goat liver twice a week and after feeding on every occasion the culture medium is changed regularly. Normally they reproduce asexually by binary fission which takes place at mid night (Ghosh 1988). The reproduction by sexual means takes place during breeding season extending from November to March. They are hermaphrodite but cross-fertilization is the rule. They produce cocoon and each cocoon liberates four to six juveniles which grow and attain maturity in course of about 30 days. The young planarians can subsist upon the prey and lead their independent life. The maintenance and culture of planarians (Fig. 1) are less expensive as they can live on goat liver/yolk of egg as ready-made food during culture and experimental work. They require careful handling during summer periods (above 32°C) when they are kept in cool temperature.

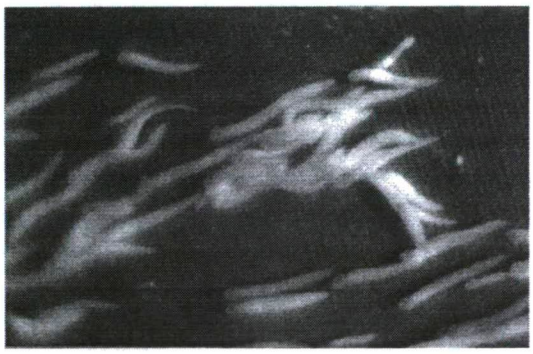

Fig. 1 Photograph showing a group of moving planarians in a culture

The different groups of mosquitoes are kept in different cisterns. They are allowed to lay eggs on the surface of the water of the tanks covered with nylon nets in the experimental condition. Mainly two groups of mosquitoes *Anopheles* and *Culex* are cultured separately. The food of mosquito larvae is the mixture of yeast and sugar, in the ratio of 5:1 and it is served at 4 to 5 days interval (Agriculture and Agri-Food Canada Insect Identification Sheet No. 86, 1983). Each life-stage/larval-stage (egg—larva—pupa) of two groups is exposed separately into large petridishes (6" diameter, depth 1") containing 7 days starved planaria in the culture medium.

Experimental design is set up into two batches. Each batch possesses three numbers of large petridishes (6" diameter, 1" depth) each one containing 5 numbers of 7 days starved matured planarians. Each life stage (egg—larva—pupa) of 50 numbers of *Anopheles* mosquitoes is exposed to the planarians of the first batch of the three petridishes separately. In the same manner, each life stage of *Culex* mosquitoes is exposed to planarians of second batch of three petridishes containing planaria. Close observation is made at each hour. It is important to note that number of larvae ingested by the planarian is measured by counting the larval exoskeleton at each hour of interval. This experiment is repeated three times for accuracy.

Result and Discussion

Continuous observation has revealed that the planarians have selective choice for the eggs/larval/pupal stages and at the same time for the different groups of mosquitoes. It has been observed that in both cases (*Anopheles* and *Culex*) larval forms are more palatable to the planarians than the other forms i.e. eggs and pupa. It also has been noticed that the planarians generally avoid very small mosquito larvae (first stage of larval form) because of their fast movement. Out of the different stages of larval forms of the mosquitoes, planarian mostly prefer 2nd and 3rd stage of larval form of mosquitoes (*Anopheles* and *Culex*) where the exoskeleton does not get so hardened as the last one (i.e. imago/adult). In the experimental set up it is noticed that five starved planaria can feed 25 number of *Anopheles* mosquito larvae within first 6 hours and the second 6 hours these planaria feed only 8 number of *Anopheles* larvae. But in case of *Culex* larvae, it has been found that five starved planaria can feed only 10 number of *Culex* larvae within first 6 hours which is very less than the intake of *Anopheles* larvae and as the time passes the feeding rate is also declines (Table 1).

Table 1. Comparison between the intake/feeding of larvae of different species of mosquitoes by five numbers of planarian (*Dugesia bengalensis*)

	1st hr	2nd hr	3rd hr	4th hr	5th hr	6th hr	7th hr	8th hr	9th hr	10th hr	11th hr	12th hr
Anopheles	12	4	1	5	-	3	-	-	4	-	3	1
Culex	6	1	-	1	-	2	-	-	-	4	-	1

Table 2 also support that consumption rate at first 6 hours of *Anopheles* larvae is much higher (52.08%) than that that of the *Culex* larvae (20.83%) by the planarians. From this observation it is clear that the planaria prefers and has a distinct choice for the *Anopheles* larvae than that of *Culex* larvae (Fig. 2). This type of food preference might be due to the larval posture (parallel to the water surface) which helps the planaria to hold or attack and capture *Anopheles* larvae easily when the hungry planaria float on the water surface. Planarians usually move by creeping on the substratum or simply by swimming or floating on the surface of the water. The *Anopheles* larvae remain in floating posture and it becomes easier for the planarians to have entrée on them. It is not clear as to why the planaria does not prefer the eggs and the pupal stages of both the mosquitoes but the disliking of pupal stage might be the harder chitinous cuticle.

Table 2. Rate of consumption of different mosquito larvae by the planarian at first and second 6 hr

	First 6 hr	Second 6 hr
Anopheles	52.08%	16.67%
Culex	20.83%	10.42%

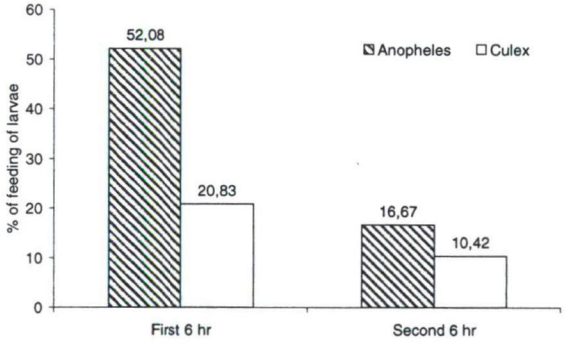

Fig. 2 Comparision of % of feeding of different type of mosquito larvae by the planarian (D. bengalensis)

The planarians had been reported to play a paramount role in maintaining the water quality in Europe (Kenk 1972). Various literatures are available in this particular field (Curtis 1902, Teshirogi *et al.* 1981, Reynoldson 1981). Kawakatsu *et al.* (1980) are of the opinion that the planarians can maintain the water quality by destroying different microorganisms, larvae of different animals including chironomids and those of a few species of mosquitoes, including *Culex*. The fasting planarians move very fast along the floor margin of the containers and very often float to the surface of the water in search of any prey (Fig. 3A). The mosquito larva is captured by the planarian which encircles (Fig. 3B) the larva strongly and inserts the proboscis through any terminal end (mouth or tail end) of the larva and sucks the entire fluid. After the meal, the planarian leaves the exoskeleton and goes down the floor of the container. Therefore, it will not be unlikely that the planarians in large number will be of great help in eradicating the mosquitoes from the locality effectively.

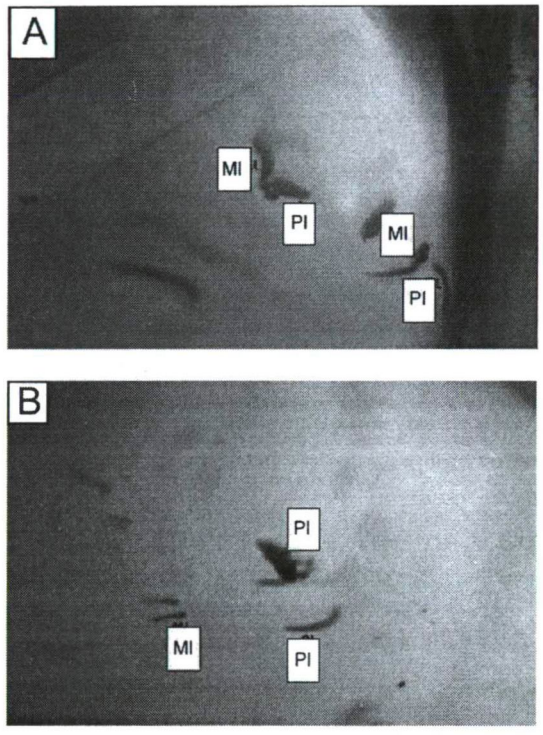

Fig. 3. Photographs showing the prey-predator relationship between mosquito larvae and the planarians; note the planaria moving towards the larva for attacking and in other it has captured the prey (A). A planarian has encircled the prey and is feeding (B). [Pl — Planaria , Ml — Mosquito larva]

The result would directly be applicable for taking remedial measure to counteract the harmful population influx of the different parasites of different disease bearing mosquitoes in the country. The surface-active agents can help to disrupt the surface forces that enable mosquito larvae to hang at the water surface, and help to reduce these the population of mosqauito larvae. Guthrie (1989) has been described the natural history of some surface-dwelling insects and outlines methods for exploring the effects on them of contaminants that alter surface forces. It has also been reported that the bacterium *Bacillus thuringiensis israelensis* is used as a mosquito control agent, sometimes in combination with a surface-active agent that helps to hold the

bacteria at the surface where the mosquito larvae will come in contact (Meritt *et al.* 1992, Clements 1992). Sih (1986) has also suggested that mosquito larvae alter their dive timing in the presence of certain predators, perhaps reduce their vulnerability by spending less time in the region where predators are most likely to find them and that this predator effect is mediated by a water-borne chemical. Such type of behaviour has not been noticed in this case. The planarians in turn are non-pathogenic, harmless, nontoxic and easy handling creatures. Kawakatsu *et al.* (1980) have also reported about the predator-prey relationship between planarians and mosquito larvae respectively. This interesting phenomenon suggests that the planarians like mosquito larvae and the small drains, and the swamp areas are ideal breeding sites of mosquitoes where planarians could easily live and multiply. The planarians become the predator of the mosquito larvae in natural condition.

The study of planaria with reference to destruction of mosquitoes at least for checking of the same is expected to have great promise to the biologists in general and people at large.

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TISCIA 34, 19-22

GENETIC (RAPD) DIVERSITY IN TWO ARMADILLIDIUM VULGARE POPULATIONS

P. Homor, I. Pfeiffer and Zs. Pénzes

Homor, P., Pfeiffer, I. and Pénzes, Zs. (2003): Genetic (RAPD) diversity in two *Armadillidium vulgare* populations. — *Tiscia 34, 19-22.*

Abstract. In this preliminary study, we investigated the effects of short-term habitat fragmentation on genetic (RAPD) diversity in two *Armadillidium vulgare* populations. Overall, the gene diversity seemed to be moderate. Genetic structure was analyzed at two levels corresponding to two spatial scales: within and between populations. Using different approaches, the overall FST=0.2 suggested genetic differentiation between the populations. The genetic structure of *A. vulgare* populations appears to have been affected by short-term habitat fragmentation.

Key words: habitat fragmentation, isolation, migration.

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Introduction

Fragmentation of natural ecosystems is generally seen to be one of the most important threats to biodiversity (Saunders *et al.* 1991, Miller *et al.* 1995). Fragmentation may occur when human activities, such as agricultural development replace large proportions of the natural ecosystem with a greatly modified matrix, within which small remnants remain. At population level, habitat fragmentation results in decreasing level of gene flow. The reduction of the population size opens the way toward the higher level inbreeding and raising the unwanted importance of genetic drift (Hartl and Clark 1997). Nevertheless, genetic processes of fragmented populations are known to be complex (e.g. McCauley 1991, Hedrick and Gilpin 1997).

The polymorphism revealed by genetic markers provides appropriate resolution for studying population structure (e.g. Sunnucks 2000). In this study, we used randomly amplified polymorphic DNA (RAPD) markers (Welsh and McClelland 1990, Williams *et al.* 1990). Partitioning RAPD variability into different levels of hierarchy, such as within and between populations is often used and considered to be a useful tool for population level studies (e.g. Huff *et al.* 1993, Liao and Hsiao 1998, Vucetich *et al.* 2001).

The aim of this preliminary study was to see whether genetic differentiation could be demonstrated for a common species of which has restricted ability of migration: 150 years of possible isolation and the distance of a few kilometers over a cultivated area can be enough to result in significant differentiation? We investigated the populations of *Armadillidium vulgare* Latreille 1804 (Crustacea, Isopoda, Oniscidae) as it was known to be a common species here. When genetic differentiation is obtained, it supports the hypothesis of isolation. But further detailed studies are needed for a clear test (see discussion).

Materials and methods

Sampling

Two grassland fragments located in the vicinity of the village Ásotthalom were selected for sampling. These sites are separated by cultivated area (about 5 kilometers). Cultivation is generally dated to be at least 150 years old. The selected species, *A. vulgare* can be characterized by limited capability of migration and sensitivity for

insecticides (Paoletti and Hassal 1999). Although the size of the fragments differs considerably, it was ignored in the analysis. *A. vulgare* populations of the two fragments are denoted by Pop1 and Pop2, where Pop2 is larger.

Individuals were collected in 2002 using pitfall traps. 12 – 36 traps arranged in 1 – 3 regular grid worked for two weeks in the three sampling occasions in both sites. 15 individuals from Pop1 and 30 from Pop2 were used for DNA extraction. The collected individuals were stored in SB puffer (25 mM NaCl, 10 mM Tris-HCl pH 8.2, 1 mM EDTA) at –20 oC, before the preparation. Each individual was handled separately.

DNA extraction and PCR amplification

DNA extraction was performed form the internal organs with the exception of the digestive tract using the GeneElute Mammalian Genomic Kit (Sigma). We followed the instructions of the manufacturer. 20 decanucleotide primers (Carl Roth GmbH) were screened for the suitability for RAPD amplification. Three of them (R2: 5'-TGCCGAGCTG-3', R11: 5'-CAATCGCCGT-3', R12: 5'-TCGGCGATAG-3') with the best amplification results were used in the following study. Reproducibility was tested only for the R2 primer. Altogether, 20 polymorphic bands were obtained for the statistical analysis (Table 1).

The PCR reaction was performed in a total volume 20 µl. The reaction mixture contained 2 µl 10x Taq-puffer, 2 µl 2.5 mM MgCl2, 2-3U Taq-polimerase (ZENON Biotech), 0.4-0.4 µl from each dNTP (10 mM, Sigma), 11.2 µl Millipore distilled water, 2 µl primer (10 pmol/µl), and 1 µl template DNA. PTC-100TM Programmable Thermal Controller (MJ Research Inc, USA) was used with the following temperature profile: 94 oC for 2 min; 35 cycles of 94 oC for 1 min, 35 oC for 1 min, 72 oC for 1.5 min.

Amplification products were separated by 1.5% agarose gel electrophoresis (70 mV, 2.5 h) and visualized by ethidium bromide staining. Lambda pUC mix (MBI Fermentas) was used as a molecular weight marker. After digitalization, the banding pattern was scored by eye. The presence of the selected bands was recorded (UVP, Biodoc-ItTM System).

Statistical analysis

Clearly, one individual should be enough for many different PCR assay. Because of technical troubles, one individual was analyzed by 1-3 primers. In this manner, statistical evaluation was performed separately on the banding pattern of the same primer. This might have some consequences besides the fact that the analysis was less effective. First, statistical power of discrimination may decrease by combining the results of the tests. Second, results obtained for the different primers are not independent as sometimes the same individual is used in different assays. Ignoring this fact may increase the magnitude of the standard error resulting in false negative decision. Nevertheless, these precautionary facts do not ignore our results as selected methods are very robust (randomization tests) and significant results are obtained (see below).

Statistical analysis was conducted with the assistance of Arlequin software (Schneider *et al.* 1999) and R (Ihaka and Gentleman 1996). RAPD method results in multilocus banding pattern with dominant marker inheritance. We used two approaches for evaluation: banding pattern is considered as a RAPD haplotype (haplotype-based approach) or a band is considered as a locus with dominant allele present (allele-based approach).

Haplotype-based statistical analysis was performed on the full data set. In order to reduce bias, allele-based methods were applied on a data set restricted by the Lynch-Milligan (1994) criterion (Table 1). Applying this condition, 14 loci were obtained and dominant allele frequencies were estimated. These were used then for estimating gene diversity (that is the expected heterozygosity under Hardy-Weinberg equilibrium) implementing the formulae of Lynch and Milligan (1994) in R. Averaging over loci, within population gene diversity can also be estimated. Owing to the lack of information about the level of inbreeding, it was assumed to be zero.

To quantify regional and local genetic structure, we examined genetic variation within and between populations using analysis of molecular variance (AMOVA, Excoffier *et al.* 1992) and fixation indices. First, AMOVA was performed on RAPD haplotypes using Arlequin. The distance between two samples was given by the number of non-shared markers (Excoffier *et al.* 1992). Between populations variance component was converted to FST and tested using 5040 random permutations. Second, the differentiation of the two populations was tested by the Raymound and Rousset method (1995) implemented in Arlequin. It is based on the null hypothesis of panmixia and gives the probability of non-differentiation. It is a nonparametric method, a Monte Carlo approximation of the extended Fischer's exact test. We used 5000 Markov chain steps during the calculations. Third, fixation indices (FST) were calculated in two different ways. FST was given from the gene diversity according to

Table 1. Summary of the sampling and within populations statistics. N stands for the sample size. Shared haplotype means the number of haplotypes can be found in both populations and shared-N is the number of individuals characterized by the shared haplotype in the given population. AMOVA shows the within population variance component given also in the percent of total variance. LM notes the number of loci satisfying the Lynch-Milligan criterion used in the diversity calculations. Variance gives the sampling variance of gene diversity.

Populations		N	Haplotype (shared, N)	AMOVA (%)	Locus (LM)	Gene diversity (variance)
R2	Total	37	19 (1)	1.351 (72.42)	7 (4)	0.30 (0.018)
	Pop1	10	8 (N=1)			0.17 (0.002)
	Pop2	27	12 (N=1)			0.44 (0.002)
R11	Total	27	16 (1)	1.145 (70.21)	7 (5)	0.28 (0.008)
	Pop1	6	5 (N=1)			0.20 (0.001)
	Pop2	21	12 (N=1)			0.37 (0.007)
R12	Total	40	13 (3)	0.793 (98.56)	6 (5)	0.17 (0.002)
	Pop1	30	11 (N=16)			0.21 (0.003)
	Pop2	10	5 (N=7)			0.12 (0.001)
Combined	Total	114	48 (5)	-	20 (14)	0.25 (0.003)
	Pop1	46	24 (N=18)			0.19 (0.001)
	Pop2	58	29 (N=9)			0.30 (0.003)

Table 2. Genetic differentiation measured by the two interpretations of FST, the between population variance and gene diversity. Allele-based results are not tested. Non-diff. stands for the p value of the Raymond-Rousset test. The estimation of the error on the calculation of p values is also given. Overall sample X2 is tested on $\chi 2$ (6 degrees of freedom), used for overall testing of differentiation (Fischer's method, Sokal and Rohlf 1995). See Table 1 for simple sizes and within group diversity and variances. NS: $p > 0.05$; ***: $p<0.001$; *: $0.01<p<0.05$;

Primer	AMOVA (%)	FST (haplotye)	Non-diff. p (error of p)	Gene diversity	FST (allelic)
R2	0.515 (27.58)	0.276***	0.000*** (0)	0.130	0.299
R11	0.486 (29.79)	0.298***	0.0259* (0.0068)	0.054	0.159
R12	0.012 (1.44)	0.0144NS	0.306 NS (0.0184)	0.004	0.022
Combined	-	X2=39.629***	X2=28.096***	0.058	0.189

Lynch and Milligan (1994). On the other hand, FST was derived from the AMOVA calculations (haplotype-based). We considered allele-based estimates only on qualitative manner.

Overall conclusion based on the haplotype approach was obtained using the Bonferroni and Fischer methods with overall significance level of 0.05. Even the classical Bonferroni method is considered to give good results when the number of tests is small (three in our case) (Rice 1995). Fischer's technique combines the probabilities of different tests of significance (Sokal and Rohlf 1995).

Result

Gene diversity of the two populations differed considerably, showing larger value for the larger population (Table 1). However, this difference should be interpreted carefully according to the unbalanced samples sizes. Nevertheless, the relatively high number of haplotypes suggests high level of diversity in both populations (not tested). For example, in the case of R2 primer in Pop1 10 individuals carry 8 unique RAPD haplotypes (Table 1).

The number of shared haplotypes between populations suggests also high level of genetic differentiation. One individual was found in both populations what shared the same haplotype in the case of R2 primer (Table 1). However, this trend varied. AMOVA carried out on the full data set showed high level of differentiation, with high values of FST for primers R1 and R2 (0.276 and 0.298, respectively, Table 2). As these were highly significant, the overall test was also significant for both of Bonferroni and Fischer methods (Bonferroni: $p<0.001$ for R2, therefore overall $p<0.003$; for Fischer's method see Table 2.). In case of primer R12, two common shared haplotype detected. This was found in 21 individuals altogether. Using Raymound-Rousset method similar conclusions were obtained. High level of differentiation was found (Table 2). Trends revealed by the allele-based methods were also similar (not tested).

Discussion

Armadillidum vulgare is generally considered to be a good "indicator species" (Paoletti and Hassal 1999) for studying questions of conservation.

Clearly, emphasizing a single species oversimplifies the problem as the level of polymorphism it shows depends on many factors, including biotic ones. Nevertheless, *A. vulgare* seems to be very variable at molecular level. In a world wide study using enzyme polymorphism of *A. vulgare*, Garthwaite *et al.* (1995) reported high level of genetic variability within and between populations, especially in Europe. Similar result was obtained in a smaller spatial scale using genetic markers (Rigoud *et al.* 1999) as it was also suggested by our results.

Further evidences are provided for the huge list of detrimental effect of human activity for natural populations. The Hungarian Great Plain, where our sampling sites are located is not an exception; 150 years of agricultural activity may isolate grassland fragments completely in a short spatial scale.

Finally, the explanation based on isolation of populations is only one possibility. Many background processes can explain differences in genetic composition of populations. Genetic markers are useful for providing high level of polymorphism but (usually) the background processes remain unclear. The effect of migration (the lack of isolation) is to eliminate differences between populations (e.g. Hartl and Clark 1997). But it takes time. Ancestral differences traced back to the foundation (the time of fragmentation) or subsequent historical events (bottle neck) may explain current differences even the lack of complete isolation. Genetic differences can be generated on many different ways. High level of differences can be interpreted as the sign of isolation but migration rate must be also estimated on the direct way (Bossart and Prowell 1998, Steinberg and Jordan 1998, Waser and Strobeck 1998).

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BACTERIOLOGICAL INVESTIGATIONS FROM WATER AND SEDIMENT IN THE LONGITUDINAL SECTION OF THE RIVER TISZA

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Teszárné Nagy, M., Némedi, L., Csépes, E., Bancsi, I., Végvári, P. and Szilágyi, E. (2003): Bacteriological investigations from water and sediment in the longitudinal section of the river Tisza. — *TISCIA 34, 23-32.*

Abstract. In 30th January, 2000 the dam of the clarifying plant of an Australian-Romanian mining-company named Aurul Corporation located on the border of Zazár settlement near to Nagybánya was broken through and more than 100,000 m^3 cyanide-containing water polluted with metal-complex had got into the Szamos through Lápos-stream then finally into the Tisza. According to the calculations referring to the turnover of substances the whole amount of about 105-110 ton cyanide remained in aqueous phase and together with attached heavy metals it left Hungary at the exit of polluting wave. The Ministry of Environmental Protection has elaborated a program of investigation for surveying the environmental and natural damages of the Szamos and the Tisza caused by cyanide pollution originated from Romania. The organic part of this program was the investigation with laminar stream performed in the longitudinal section of the Tisza which happened between 19th and 30th September in 2000 at the whole Hungarian reach of the Tisza from Tiszabecs to Tiszasziget. Bacteriological examinations were performed from water and sediment. In the seventh month after marching down of pollution the hygienic bacteriological state of water of the Tisza developed according to the characteristics of the autumn state with low water. The effect of cyanide pollution on the aquatic communities of microbes has not been already detectable. However, the results of bacteriological investigations with the character of material-cycles can be considered as a basic research on the Hungarian reach of the river Tisza.

Keywords: cyanide pollution, microbial cycles of elements, sampling with laminar stream.

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Introduction

In 30th January, 2000 at 22 o' clock the dam of the clarifying plant of an Australian-Romanian mining-company named Aurul Corporation located on the border of Zazár settlement near to Nagybánya was broken through and more than 100,000 m^3 cyanide-containing water polluted with metal-complex had got into the Szamos through Lápos-stream then finally into the Tisza. In the case of total dissolved cyanide-content we can tell about the concentration-relations developed during the time of marching down of pollution that the maximum concentration was between 20 and 30 mg/l in the Szamos, between 10 and 15 mg/l at the reach of the Tisza located under the Szamos and then moving downstream this concentration gradually decreased. The maximal concentration in water leaving Hungary was 1.49 mg/l (which was still 150 times higher than the permissible value). Metal-complexes — well soluble in water — come with polluting wave were very stable. In consequence of this the whole amount of about 105-110 ton cyanide remained in aqueous phase according to the calculations referring to the

turnover of elements and together with attached heavy metals it left Hungary at the exit of polluting wave. (This fact was also verified by the results of samples taken at the reservoir of Vaskapu).

In the February of 2000 the Ministry of Environmental Protection elaborated a program of investigation (with the collaboration of concerned Environmental Protection Inspectorate, National Parks, the Water-quality Protection Institute of VITUKI Corporation and KGI) titled: "Surveying the environmental and natural damages of the Szamos and the Tisza caused by cyanide pollution originated from Romania". The implementation of the program consisted of three phases. In the first phase the tracking of pollution marched down and laboratory measurements had been done as well as the estimation of the extent of destruction appearing in the communities of living organisms had been started. In the second phase the surveying of the extent of damage caused by polluting material marched down had taken place as well as the project of the investigation performed in the longitudinal section of the Tisza had been created. According to this the expedition would be performed in the period of low water at the Hungarian reach of the Tisza form the national boundary to the national boundary. The work of the expedition was planned for the period of two weeks which would be repeated in every two or three years. For the third phase the Ministry has planned the investigation of the regeneration of aquatic communities of living organisms, the reduction of detected irreversible damages and the implementation of a rehabilitating program.

The organic part of this program was consequently the investigation with laminar stream performed in the longitudinal section of the Tisza which happened between 19th and 30th September in 2000.

The client was the Ministry of Environmental Protection, the executor was the Middle-Tisza Water Authority. Chemical and biological processing of samples were performed by the following institutes: Budapest Institute of the National Public Health and Medical Officer Service (Hungarian abbreviation: ÁNTSZ), Department of Public Health Biological Laboratory (Budapest); Ecological Department of Debrecen University (Debrecen); Fish-culture Research Institute (Szarvas); North Hungarian Environmental Inspectorate (Miskolc); Environmental Inspectorate of Upper-Tisza Region (Nyíregyháza), Environmental Inspectorate of Trans Tisza (Debrecen); Environmental Inspectorate of the Middle-Tisza Region (Szolnok), Middle-Tisza Water Authority; Environmental Inspectorate of Lower Tisza Region (Szeged); VITUKI Corporation (Budapest); MTA ÖBKI — Hungarian Danube Research Station (Göd); Eszterházy Károly College (Eger); Biological Department of Szeged University (Szeged).

Review of literature

During last thirty years the Middle-Tisza Water Authority (MTWA) has performed investigations with laminar stream performed in the longitudinal section of the Tisza in many occasions. In six occasions (June of 1975, September of 1975, August of 1977, September of 1979, September of 2000, November of 2002) the sampling of the whole Hungarian reach of the Tisza has happened from which the majority was a sampling with laminar stream. During each expedition the sampling of water (and sediment in some cases) has happened at 30 to 50 sampling sites. On the occasion of single investigations performed in the longitudinal section of the river the majority of sampling sites was the same. In the seventy' years biological examinations also have been performed beside physical and chemical examinations of water and sediment. The aim was to determinate those parameters among microbiological ones which were examined in the hygienic routine. The authors published the results of measurements in the volumes of Tiscia (B. Tóth 1981, Estók 1980, 1981, Hegedűs and Zsikó 1981). In the autumn of 2000 the microbiological examinations had been extended also to the microbiological parameters which are important from the aspect of material-cycles of the sediment of the Tisza and its tributaries.

Necessity of material-flow investigations performed on the basis of bacterial activity

In the latter years Hungarian bacteriological research and the applied, routine bacteriological activity have found themselves face to face with fundamental methodological challenge and a challenge in the interpretation. A continuous change can be experienced in the terminology of environmental bacteriology. Today we do not distinguish so sharply the autochthonous and allochthonous microbiota discussed and examined separately earlier as e.g. in receiving water bodies the one part of the allochthonous microbiota originated from sewage waters can infiltrate into the functional microbe-community of a given surficial water.

According to Némedi (Gorzó *et al.* 1998), we ought to classify the elements of microbiota (taxa, taxon-groups) on the basis whether they have a

function in the place of detection, or this activity is occasional only, or they do not have any role at all in the material-cycles of a given medium. The same taxon can be found on either side so in this relation. The function is decisive not the classification into a species. Certain taxa have shown activity of material-cycles very widely noting also that bacteria showing obligate function can occur too. Thus the 'microbiota elements' of public health can already be well embedded in the general structure of microbial material-cycles.

Though the quantitative examination of bacteria receives lots of criticism (differences of in vivo/in vitro circumstances), yet the determination of actual number of microbes is a very important question of environmental microbiology. There is every hope that the extent of bacterium-density, which is necessary for producing a given function (activity), would be traceable by using more reliable methods.

However, today there are limits yet in the knowledge of qualitative composition (soil, river, lake) with whole level of species. There are such micro-organisms presence of which can be detected by electron microscope, but they can not be cultured in any medium (oligotrophic microbes). However, one part of microbes, which can be cultured, is undeterminable (according to the present-day state of taxonomy). However, we have to take into consideration the fact, too, that during the annual dynamics the composition of microbiota is also changing, thus it is understandable that the tracking of population dynamics in qualitative level can mean insoluble task many times. However, by spreading the use of molecular methods and by appropriate use of automatic identifying systems of microbes we can get closer to the answer of the question.

Materials and Methods

The investigation of the Tisza performed in the longitudinal section was implemented between 19th — 30th September, 2000. The expedition sampled the Tisza and its tributaries (the Szamos, the Lónyai-channel, the Bodrog, the Sajó, the Zagyva, the Hármas-Körös, the Maros) from Tiszabecs (744.2 r.km) to Tiszasziget (167.0 r.km) altogether at forty sampling sites form the board of an exploratory ship (Table 1).

The bacteriological processing of forty water-samples taken from the channel line was performed in the Regional Laboratory of MTWA and the laboratory of the Budapest Institute of ÁNTSZ, Department of Public Health Biological Laboratory. The sampling of sediment happened at forty sections, tree samples were taken per sections (right bank, left bank and channel line). So altogether 120 sediment-samples were collected for physical, chemical, heavy-metal and macro-zoobenthos examinations. From this collection in the case of 19 sediment-samples the Budapest Institute of ÁNTSZ, Department of Public Health Biological Laboratory performed the microbiological examinations important from the aspect of material-cycles.

In this paper we report particularly on microbiological relations of the investigation performed in the longitudinal section of the Tisza in 2000.

Bacteriological examinations performed at forty water-samples taken from channel line: Aerobe total count at 22 and 37 °C, number of Coliforms MPN, number of Faecal Coliforms MPN, number of Fecal Streptococci CFU, number of Clostridia CFU at 46 °C, total number of bacterial CFU (Accridin Orange Direct Count method, Hobbie *et al.*, 1977).

Bacteriological examinations performed at seven water-samples taken from channel line: Determination of *Salmonella*-positivity, *Escherichia coli* and *Pseudomonas aeruginosa*.

Bacteriological examinations performed from 19 sediment-samples: Determination of number of Coliforms CFU, number of Faecal Coliforms CFU, number of Fecal Streptococci CFU, number of Clostridia CFU, *Salmonella*-positivity, *Pseudomonas aeruginosa*, aerobe and anaerobe total count at 22 and 37 °C, *Staphylococcus aureus*, number of colonies indicating proteolytic activity, Mould-fungus CFU, Yeast-fungus CFU, total count of Desulphurylating bacteria, total count of Cellulolytic bacteria, total count of Ammonifier bacteria, total count of Nitrifier bacteria, total count of Denitrifier bacteria.

Bacteriological qualification was performed according to the C group of the Table 2 of MSZ 12749:1993 standard and on the basis of the guide of the Budapest Institute of ÁNTSZ, Department of Public Health Biological Laboratory.

Results

Water-bacteriology

Number of saprophyte bacteria CFU indicates the extent of bacterium-biota which depends on the presence of quickly decomposable organic materials and decomposes those materials.

Viable microorganisms existing in water reproduce generally better at 22 °C, than at 37 °C in the mediums used in laboratories.

Microorganisms reproducing at 37 °C (which get into our waters with external pollution) are less viable in water. They are trend-like indicators of

Table1. CFU and Coliform counts from the longitudinal section of Tisza performed between 21st and 30th September, 2000.

Time of sampling	Name of the water body	r.km	Total count at 22°C, CFU/ml	Total count at 37°C, CFU/ml	Number of Coliforms in 1 ml
20.09.2000	TISZA	744.2	1 300	740	17
20.09.2000	TISZA	687.0	640	380	4.9
20.09.2000	Szamos	1.0	28 000	13 000	350
20.09.2000	TISZA	685.0	18 000	13 000	350
20.09.2000	TISZA	683.0	12 000	7 200	160
21.09.2000	TISZA	627.8	5 600	4 400	14
21.09.2000	TISZA	616.5	5 200	4 000	13
21.09.2000	TISZA	591.9	6 800	6 400	3.3
22.09.2000	TISZA	568.7	6 600	6 300	3.3
22.09.2000	TISZA	559.9	2 700	2 500	1.3
22.09.2000	Lónyai-csatorna	1.0	180 000	110 000	2 400
22.09.2000	TISZA	557.9	3 100	1 600	11
22.09.2000	TISZA	555.9	2 300	1 100	13
23.09.2000	TISZA	544.7	600	350	2.6
23.09.2000	Bodrog	1.0	480	150	3.3
23.09.2000	TISZA	542.7	880	190	1.3
23.09.2000	TISZA	523.5	1 100	900	1.7
24.09.2000	TISZA	493.4	280	120	0.68
24.09.2000	Sajó	1.0	1 800	750	7.9
24.09.2000	TISZA	491.4	250	130	0.45
24.09.2000	TISZA	489.4	400	100	0.78
25.09.2000	TISZA	464.0	400	300	1.1
25.09.2000	TISZA	453.0	220	75	0.4
26.09.2000	TISZA	431.0	8 400	4 300	3.3
26.09.2000	TISZA	415.0	20 000	160	0.78
26.09.2000	TISZA	404.0	17 000	4 000	0.78
27.09.2000	TISZA	395.0	12 000	250	2.2
27.09.2000	TISZA	336.6	11 000	900	7.0
27.09.2000	Zagyva	1.0	6 500	2 000	160
27.09.2000	TISZA	334.6	11 000	300	7.9
28.09.2000	TISZA	330.0	2 400	2 200	7.0
28.09.2000	TISZA	266.4	10 000	3 600	170
29.09.2000	TISZA	244.6	6 000	1 500	140
29.09.2000	Hármas- Körös	1.0	1 800	450	28
29.09.2000	TISZA	242.6	16 000	1 500	54
29.09.2000	TISZA	215.0	2 000	1 400	110
30.09.2000	TISZA	178.0	680	440	35
30.09.2000	Maros	1.0	1 500	1 200	22
30.09.2000	TISZA	176.0	1 800	1 200	92
30.09.2000	TISZA	167.0	3 000	2 400	160

Table 2. Faecal coliform, *Streptococcus*, *Clostridium* and planctonic bacterium counts from the longitudinal section of the river Tisza performed in between 21st and 30th September, 2000.

Time of sampling	Name of the water body	r.km	Faecal coliforms MPN/ml	Faecal streptococci CFU/ml	Clostridia CFU/ml	Planctonic bacteria million cell/ml
20.09.2000	TISZA	744.2	4.9	1.5	16	2.35
20.09.2000	TISZA	687.0	1.3	0.3	12	2.52
20.09.2000	Szamos	1.0	35.0	3.2	210	5.11
20.09.2000	TISZA	685.0	22.0	2.2	160	3.63
20.09.2000	TISZA	683.0	35.0	1.6	88	2.90
21.09.2000	TISZA	627.8	7.9	0.1	70	3.08
21.09.2000	TISZA	616.5	1.7	0.1	45	3.02
21.09.2000	TISZA	591.9	0.78	0.1	65	3.68
22.09.2000	TISZA	568.7	0.78	0.1	53	3.71
22.09.2000	TISZA	559.9	0.45	0.1	52	4.00
22.09.2000	Lónyai-cs.	1.0	920.0	60.0	1 200	10.04
22.09.2000	TISZA	557.9	1.1	0.2	96	5.34
22.09.2000	TISZA	555.9	4.9	0.0	90	4.18
23.09.2000	TISZA	544.7	0.2	0.0	60	4.29
23.09.2000	Bodrog	1.0	1.4	0.2	70	3.37
23.09.2000	TISZA	542.7	0.2	0.0	70	3.63
23.09.2000	TISZA	523.5	0.0	0.0	70	3.71
24.09.2000	TISZA	493.4	0.2	0.1	70	3.77
24.09.2000	Sajó	1.0	4.9	0.7	680	4.09
24.09.2000	TISZA	491.4	0.0	0.2	100	3.37
24.09.2000	TISZA	489.4	0.0	0.1	120	2.87
25.09.2000	TISZA	464.0	0.2	0.1	180	2.21
25.09.2000	TISZA	453.0	0.0	0.2	96	2.73
26.09.2000	TISZA	431.0	0.0	0.1	45	2.29
26.09.2000	TISZA	415.0	0.45	0.1	40	2.73
26.09.2000	TISZA	404.0	0.0	0.0	82	2.41
27.09.2000	TISZA	395.0	0.4	0.0	95	2.18
27.09.2000	TISZA	336.6	0.45	0.1	100	2.26
27.09.2000	Zagyva	1.0	7.0	7.7	960	2.90
27.09.2000	TISZA	334.6	0.45	0.1	37	2.29
28.09.2000	TISZA	330.0	4.9	0.7	110	2.32
28.09.2000	TISZA	266.4	160.0	0.7	120	2.32
29.09.2000	TISZA	244.6	92.0	0.9	180	2.41
29.09.2000	Hármas- Körös	1.0	24.0	0.4	130	2.73
29.09.2000	TISZA	242.6	43.0	0.5	100	2.93
29.09.2000	TISZA	215.0	92.0	1.0	77	2.47
30.09.2000	TISZA	178.0	17.0	0.1	65	2.50
30.09.2000	Maros	1.0	3.3	0.5	63	3.34
30.09.2000	TISZA	176.0	13.0	0.4	76	2.76
30.09.2000	TISZA	167.0	24.0	1.5	72	2.76

sewage waters with communal and agricultural origin, or rather they can indicate hygienic problem, too.

Aerobe total count at 22 and 37 °C

The aerobe total count was not significant (II. class) at the Upper-Tisza. The polluted (IV. class) Szamos with major water-discharge influenced the bacterium-biota of the Tisza to a large extent. The aerobe total count increased threefold in the Tisza downstream the mouth of the Szamos (685.0 r.km) compared to the value detected at section of 744.2 r.km (Table 2). Considering the aerobe total count at 22 and 37 °C the quality of water belonged to the III-IV. classes in this region.

Considering the number of aerobe colony forming units at 22 and 37 °C, river Tisza belonged to the II. class from the area of Gávavencsellő (559.9 r.km) to Tiszacsege (453.0 r.km) downstream the river.

From Tiszafüred (431.0 r.km) to Mindszent (215 r.km), the total count at 22 °C had a magnitude of ten thousand (III-IV. classes), the number of colony forming units at 37 °C had a magnitude of hundred (II-III. classes).

Among tributaries, Lónyai-channel was the most polluted (Table 2), the aerobe colony forming bacteria had been cultured in the magnitude of hundred thousand (V. class).

Facultative faecal-indicator bacteria having the type of *Clostridium* are sulphite-reducing anaerobe spored microorganisms which have short thick rod-like shape, form a capsule and their spores are oval-shaped. One part of them is the inhabitant of human alimentary canal, the other part lives in sediment or soil, for this very reason they are not really suitable for classifying categories in surface waters. In the case of sediment-disturbing the spores can get into water body again and being more resistant than vegetative forms they can be the indicators of former faecal pollution.

Clostridium-type bacteria were present in a great number at the whole reach of the Tisza (from 687 r.km to 167 r.km) in the water body. From water of the Lónyai-channel we have cultured these bacteria in larger amount with one order of magnitude — compared to the other tributaries.

The members of Enterobacteriaceae family are facultative faecal-indicator organisms. Their presence proves the load of organic material getting into water from outside.

The number of Coliform bacteria belonged to the II. class at river Tisza upstream the mouth of river Szamos. The high number of coliform bacteria of Szamos was measurable also at the Tisza after the moth (Table 2). This reach of the river (687-683 r.km) can be categorized into the 'polluted' category. The river can be characterized by the I-II. categories of water-quality on the basis of the number of coliform bacteria up to the area of Tiszaug (266.4 r.km) with regard to this bacterium-group. The number of bacteria has increased with two orders of magnitude at Tiszaug (probably) due to the effect of sewage water of Szolnok and it does not decrease significantly up to the area of Tiszasziget (167 r.km). Among tributaries, river Szamos and the Lónyai-channel were the most polluted.

Obligate faecal-indicators

Those coliform bacteria, which ferment lactose also at 44 °C, are faecal coliform bacteria. Obligate faecal indicators originate from faeces solely, getting into water their time for surviving is short, they are not able to post-reproduce in water. They are reliable indicators of new faecal pollution.

The habitat of faecal Streptococci is the human- and animal alimentary canal therefore their cultivation from water (together with faecal Coliforms) indicates new faecal pollution.

Faecal Streptococci are very resistant, they are able to survive in unfamiliar circumstances for a longer term.

According to this, if the number of faecal Streptococci is not accompanied — simultaneously — to the large number of faecal Coliforms then it indicates former already terminated pollution in most cases.

The obligate faecal indicators occurred in the greatest number at the reach of river Tisza (685.0-616.5 r.km) located downstream the mouth of river Szamos (Table 2). The quality of water belongs to the III-IV. classes in this water body. Faecal pollution was not significant from the area of Tuzsér to Szolnok (616.5-330.0 r.km), while the extent of pollution justified a classification into III-IV. classes from Tiszaug to Tiszasziget (266.4-167 r.km).

Among tributaries, faecal pollution of Lónyai-channel was significant.

Sometimes the total number of planktonic bacteria determined by direct microscopic counting is greater with more orders of magnitude than the number of bacteria determined by cultivating methods because there are microorganisms of which presence can be detected by microscope though, but they can not be cultivated in any kind of medium. By AODC technique the living (but it is not sure that continuing active metabolism) bacterium-cells can be counted.

Total number of bacteria (or the number of planktonic bacteria) has ranged between 2.18 × 106

cell/ml and 5.34 x 106 cell/ml at the examined reach of the Tisza. Among tributaries the number of planktonic bacteria of Lónyai-channel was the highest: 10.04 x 106 cell/ml (Table 2) which represented a significant biomass.

The Budapest Institute of ÁNTSZ, Department of Public Health Biological Laboratory has performed hygienic bacteriological examinations from water at seven sampling sites in the course of the investigation of the Tisza performed in the longitudinal section (at 687; 683; 489; 266.4; 215; 167 r.km and at the mouth of the Szamos). On the basis of these examinations *Escherichia coli* was detectable at each of seven sampling sites, in the largest number at the section of the Tisza (683 r.km) located downstream the mouth of the Szamos (21 000 colony/100 ml).

Salmonella-positivity was detectable in the Szamos, the presence of *Pseudomonas aeruginosa* was demonstrable only in the sections of river Tisza upstream (687.0 r.km) and downstream (683.0 r.km) the mouth of river Szamos.

Sediment-bacteriology

As the Hungarian Standards valid at the present do not determine a limit-value for the quantitative relations of bacterium-communities living in the sediment therefore the assessment has happened only on the basis of trend-lines fitted to the diagrams.

Examination of hygienic parameters

According to the bacteriological results of the Budapest Institute of ÁNTSZ, Department of Public Health Biological Laboratory the aerobe total count at 22 and 37 °C was present in the magnitude of ten thousand while the anaerobe total count (at the two same degrees of temperature) in the magnitude of thousand in the sediment of the section of river Tisza from 568.7 r.km to 493.4 r.km (Tiszabercel – Tiszagyulaháza).

The number of these bacteria has decreased significantly in the sediment-samples of the Middle-Tisza, while the aerobe and anaerobe total counts of sediment have increased threefold at the Lower-Tisza from the area of Tiszaug to Tiszasziget (266.4 - 167.0 r.km). Among tributaries, the aerobe and anaerobe total counts of the sediment of rivers Hármas-Körös and Szamos were high outstandingly.

Number of Clostridia exceeded one thousand in the sediment originated from the reach of Upper-Tisza (559.9 – 491.4 r.km) which, however, decreased significantly at the Middle- and Lower-Tisza. The number of colony (7500 colony/g wet sediment) in the sediment of the Lónyai-channel has indicated a former pollution with large probability.

The number of Coliform bacteria was surprisingly small in the sediment-samples of Tisza. Their number does not exceed the value of 100/g wet sediment in each case.

The sediment of the Lower-Tisza (266.4 – 167 r.km) proved to be the most polluted.

Among tributaries, river Sajó had the best quality considering the number of Coliform bacteria.

Faecal pollution of sediment was not significant at the examined reach of Tisza. The number of faecal Coliforms and the number of faecal Streptococci were larger in the area of Tiszaújváros at the Upper-Tisza (491.4 r.km), then they decreased at the Middle-Tisza. The number of faecal indicators had increased again in the area of Tiszaug (266.4 r.km).

Among tributaries, the sediment of Lónyai-channel and Hármas-Körös was very polluted by microorganisms originated from faeces.

Salmonella- and *Staphylococcus aureus*-positivity was not demonstrable in the 19 sediment-samples.

Pseudomonas aeruginosa-positivity was detected in four cases by the Budapest Institute of ÁNTSZ, Department of Public Health Biological Laboratory in the sections of Tisza located at 559.9; 336.6; 215.0 and 167.0 r.km.

Quantitative relations of microbiota elements participating in the microbial cycles of elements in river-sediments

Aquatic plants rich in cellulose die in water and sink down to the bottom, sewage waters getting into the river also can contain by-products with cellulose content (e.g. sewage water of a paper-mill) which are decomposed by the activity of cellulose-decomposing bacteria, ray-fungi and fungi.

The amount of Cellulose decomposers (Table 3) is significant in the sediment of the Upper-Tisza from the area of Gávavencsellő to Tiszaújváros (559.9 – 491.4 r.km). This amount has decreased significantly at the Middle-Tisza, then it has increased slightly downstream the mouth of the Zagyva after the entering of sewage water of the Paper-mill of Szolnok.

The largest amount of cellulose decomposers was demonstrable in the sediment of the Lónyai-channel and river Bodrog (Table 3).

Bacteria indicating proteolytic activity participate in the process of proteolysis occurring in the course of biodegradation. During proteolysis amino-acids are produced as final products of lytic proteins.

The total count indicating proteolytic activity has increased threefold in front of the mouth of Lónyai-channel (559.9 r.km) and has reached the magnitude of hundred thousand to the area of Tiszatardos

3. Table: Results of sediment-bacteriological examinations of the investigation of the Tisza performed in the longitudinal section of the river (in 1 g wet sediment).

Name of the water body	r.km	1.	2.	3.	4.	5.	6.	7.	8.	9.
TISZA	744.2	-	-	-	-	-	-	-	-	-
TISZA	687.0	9.3	100000	9.3	4.3	24	10	3000	600	0.0
Szamos	1.0	24	100000	9.3	0.3	24	35	2500	0.0	0.0
TISZA	685.0	-	-	-	-	-	-	-	-	-
TISZA	683.0	12	100000	9.3	0.3	24	30	5000	100	0.0
TISZA	627.8	-	-	-	-	-	-	-	-	-
TISZA	616.5	-	-	-	-	-	-	-	-	-
TISZA	591.9	-	-	-	-	-	-	-	-	-
TISZA	568.7	>1100	100000	>110	24	>110	2000	25000	800	700
TISZA	559.9	>1100	100000	46	1.5	110	300	60000	600	800
Lónyai-cs.	1.0	>1100	100000	>110	9.3	110	7500	60000	100	0.0
TISZA	557.9	-	-	-	-	-	-	-	-	-
TISZA	555.9	-	-	-	-	-	-	-	-	-
TISZA	544.7	>1100	100000	110	24	>110	1500	200000	700	0.0
Bodrog	1.0	>1100	100000	>110	110	>110	1125	200000	1500	0.0
TISZA	542.7	-	-	-	-	-	-	-	-	-
TISZA	523.5	>1100	100000	110	46	>110	1375	80000	800	0.0
TISZA	493.4	29	100000	110	110	1.5	750	10000	500	0.0
Sajó	1.0	46	100000	14	2.3	2.3	50	4000	0.0	0.0
TISZA	491.4	-	-	-	-	-	-	-	-	-
TISZA	489.4	-	-	-	-	-	-	-	-	-
TISZA	464.0	>110	100000	9.3	4.3	2.8	37	4000	0.0	0.0
TISZA	453.0	-	-	-	-	-	-	-	-	-
TISZA	431.0	-	-	-	-	-	-	-	-	-
TISZA	415.0	-	-	-	-	-	-	-	-	-
TISZA	404.0	>110	100000	9.3	4.3	15	150	9000	0.0	0.0
TISZA	395.0	-	-	-	-	-	-	-	-	-
TISZA	336.6	1100	100000	110	24	>110	97	20000	0.0	0.0
Zagyva	1.0	-	-	-	-	-	-	-	-	-
TISZA	334.6	-	-	-	-	-	-	-	-	-
TISZA	330.0	-	-	-	-	-	-	-	-	-
TISZA	266.4	>1100	100000	46	4.3	10000	50	10000	500	0.0
TISZA	244.6	-	-	-	-	-	-	-	-	-
Hármas- Körös	1.0	>2400	100000	46	9.3	10000	450	100000	800	0.0
TISZA	242.6	-	-	-	-	-	-	-	-	-
TISZA	215.0	>1100	100000	24	24	10000	122	100000	400	0.0
TISZA	178.0	-	-	-	-	-	-	-	-	-
Maros	1.0	>4600	100000	46	24	100000	650	200000	500	0.0
TISZA	176.0	-	-	-	-	-	-	-	-	-
TISZA	167.0	>2400	100000	21	4.3	10000	800	80000	300	0.0

Key to the signs used : 1.: Heterotrophic H_2S producers MPN/ml, 2.: Ammonifying bacteria MPN/ml, 3.: Cellulose-degrading bacteria MPN/ml, 4.: Nitrifying bacteria MPN/ml, 5.: Denitrifying bacteria MPN/ml, 6.: Clostridia CFU/ml, 7.: number of colony indicating proteolytic activity CFU, 8.: CFU of mould fungi, 9.: CFU of yeast fungi

(523.5 r.km). The number of these microbial elements has decreased at the Middle-Tisza (Table 3), and the total count indicating proteolytic activity has increased to the magnitude of hundred thousand only downstream the mouth of Hármas-Körös. We have managed to detect these colonies in the largest number from the sediment of rivers Bodrog and Maros.

Chemolithotroph Nitrifying bacteria oxidize the large part of ammonia found in water through nitrite to nitrate and they assimilate carbon dioxide by the help of obtained energy. The most frequent nitrite-forming microorganisms are the members of the

genera *Nitrosomonas* and *Nitrosococcus*. Nitrate is produced as a result of the activity of the members of the genus *Nitrobacter*. Nitrate produced during nitrification has a great importance. Algae and higher plants assimilate nitrate in a large mass, and the denitrifying bacteria utilize nitrate as electron-acceptor.

The number of nitrifying bacteria was the largest in the sediment at the reach of the Upper-Tisza located between Tiszabercel and Tiszagyulaháza (568.7 – 493.4 r.km). Their amount has decreased at the Middle-Tisza, then their number has increased slightly (Table 3) in the area of Szolnok - Mindszent (336.6 – 215.0 r.km). Among tributaries, the number of nitrifying bacteria reached the magnitude of hundred in the sediment of river Bodrog.

Denitrifying organisms reduce nitrite produced in the first step of nitrate-reduction to elemental nitrogen. Organisms performing denitrification do not belong to a uniform group neither morphologic nor biochemical way. Denitrification can be performed by e.g. the members of the genus *Bacillus*, certain genera of the family Micrococcaceae, *Pseudomonas aeruginisa, Thiobacillus denitrificans* and so on. The small amount of dissolved oxygen, abundant nitrate and organic material refer to the presence of denitrifiers.

Denitrifying organisms can utilize the most diverse materials (e.g. the intermediate products of cellulose-decomposition) as electron donor.

The number of denitrifiers reached the multitude of hundred in the sediment-samples taken at the reach of the Upper-Tisza located between 568.7 and 523.5 r.km (Table 3), then their number has decreased significantly at the reach of the Middle-Tisza. Denitrifiers were present in a huge amount (in the magnitude of ten thousand) in the sediment-samples of the area located between Tiszaug and Tiszasziget (266.4 – 167.0 r.km). Among tributaries, mainly the sediment of rivers Maros and Hármas-Körös contained these microbiota elements in the largest number.

The total count of mould fungi was the largest in the sediment-samples taken at the reach of the Upper-Tisza located between Tiszabercel and Tiszagyulaháza (568.7 – 493.4 r.km). The amount of mould fungi was not considerable at the Middle-Tisza. The total count of mould fungi has increased to the magnitude of hundred at the reach of the Lower-Tisza located on the area of Tiszaug and Tiszasziget (266.4 – 167.0 r.km).

Among tributaries, we managed to isolate mould fungi in the largest number from the sediment of the Bodrog (Table 3).

Yeast fungi were demonstrable only in two sediment-samples of the reach of the Upper-Tisza (568.7; 559.9 r.km). We have not managed to culture these fungi in the sediment-samples of the Middle- and Lower-Tisza.

Table 3. contains the data referring to the amount of desulphurylating and ammonifying bacteria. However, as the results of measurements are only approximate, therefore they have not been suitable for drawing a diagram.

Discussion

From the results we can conclude that after marching down of pollution in the seventh month the hygienic bacteriological state of water of river Tisza developed according to the characteristic of the autumn state with low water. The effect of cyanide pollution on the aquatic communities of microbes has already not been demonstrable.

According to the hygienic water-bacteriological examinations, the Upper-Tisza located upstream the mouth of the Szamos belongs to the I-II. classes. Downstream the mouth of the Szamos (Gergelyiugornya – Záhony), each examinations with regard to hygienic bacteriological group belong to the IV. class ('polluted').

At the following reach of the river (Záhony – Tiszafüred), water quality is of I-II classes. On the basis of the number of aerobe organic-material decomposers water belongs again to the III-IV. classes from Tiszafüred to Tiszaug. In the area of Tiszaug – Tiszasziget the quality of the Tisza is of III-IV. classes according to every bacterium-group. The section located downstream the mouth of river Szamos (Gergelyiugornya – Vásárosnamény) and the section of Tiszaug – after receiving sewage water of Szolnok – are very polluted by faecal way.

Among tributaries of the Tisza, the Lónyai-channel and the Szamos were the most polluted from hygienic bacteriological point of view. Positive activity of *Salmonella* was detectable in the Szamos. *Pseudomaonas aeruginosa* was only demonstrable from the sections of the Tisza located upstream (687.0 r.km) and downstream (683.0 r.km) the mouth of the Szamos.

The results of bacteriological examinations with the character of material-cycles, performed from sediment are considered as a basic-research at the Hungarian reach of river Tisza. Namely, in the course of the investigation of Tisza performed in its longitudinal section in 1979 only the hygienic bacteriological examination of sediment took place.

According to the results of bacteriological examination of sediment performed in 2000, the

bacterium-groups having importance from both hygienic aspect and the aspect of material-cycles were present in a huge number at the reach of the Upper-Tisza (Gávavencsellő – Tiszaújváros). The amount of the microbiota elements of sediment has decreased in the Middle-Tisza, while the hygienic bacteriological parameters were the most disadvantageous at the Lower-Tisza and the presence of such a bacterium-biota was detectable which had been working increased way from the aspect of material-cycles. According to the results of hygienic bacteriological examinations performed from the sediment of the tributaries, the sediment of the Lónyai-channel, Hármas-Körös and Maros proved to be the most polluted. The microbiota elements participating in the microbial cycles of elements were the most active in the sediments of rivers Hármas-Körös, Bodrog and Maros.

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TISCIA 34, 33-39

AGE- AND DENSITY DEPENDENT SURVIVAL IN A YELLOW-NECKED WOOD MOUSE *APODEMUS FLAVICOLLIS* (MELCH.) POPULATION OF A FOREST HABITAT

Gy. Horváth and Z. Wagner

Horváth, Gy. and Wagner, Z. (2003): Age- and density dependent survival in a yellow-necked wood mouse *Apodemus flavicollis* (Melch.) population of a forest habitat. — *Tiscia 34, 33-39.*

Abstract. A 10-month live trapping investigation was carried out in a *Querco robori-Carpinetum* habitat in south-Hungary in 1997. During a total of 6050 trap-nights with 5-night sessions, 306 *A. flavicollis* individuals were captured and marked, and for their demographic parameters, age-dependent survival models were tested using the JOLLYAGE program. The estimators in the program recorded a September population maximum for *A. flavicollis*. Adults had significantly higher survival rates which decreased as the population grew. Survival probability and capture probability were significantly correlated with age. Based on goodness-of-fit tests our data fitted all three models of JOLLYAGE; the group of age-dependent models proved to be appropriate for our *A. flavicollis* capture data. A comparison of the models revealed that the general model A2 rejected B2 which is reduced in its calculation of survival rate, but it did not reject model D2 which uses constant capture and survival probability. Accordingly, based on our model selection results we consider the simplest D2 model with reduced parameters to be the most appropriate.

Keywords: Apodemus flavicollis, survival analyses, age-dependence, JOLLYAGE

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Introduction

The "life-history" analysis of the subject species of the present study (e.g. Gliwicz *et al.* 1968, Bujalska *et al.* 1968, Bujalska 1975), as well as several case studies published in this field and presenting results primarily about *Peromyscus* species (Wolf 1986, Millar 1989, Duquette and Millar 1995) and New-World *Microtus* species (Mihok 1984, Boonstra 1989) showed that variations in the fitness in a population is basically determined by variations in fecundity, survival, or both (Lebreton *et al.* 1992). The probability of survival is influenced, on the one hand, by characteristics of the individual such as age, sex, weight, genotype and phenotype, and, on the other hand, by abiotic environmental variables together with inter- and intraspecific competition and predation. It is, thus, important in testing an ecological hypothesis to use estimates of survival so as to better understand the dynamics of a studied population (Lebreton *et al.* 1992). It is essential to test for possible variation in survival and capture rates among different age groups (Pollock 1981).

Regarding small mammals, in Europe it was Paradis *et al.* (1993), using the program SURGE, to analyse sex- and age-dependent survival of the Mediterranean pine vole (*Microtus duodecimcostatus*). Also, Paradis and Croset (1995) looked at to what degree the demographic changes in a habitat were determined by "source-sink" dynamics. Different survival rates have been shown to exist in habitats differing in food availability (Paradis 1995).

In a population of *A. flavicollis* Bobek (1973) analysed the effect of density on survival, based on data from trapping in a *Tilio-Carpinetum* forest habitat. He demonstrated a decrease in survival rates at high population density. He also found that mortality rates decreased with increasing age. Earlier investigations proved that reproductivity, abundance and, through these, population dynamics are determined by habitat structure and concordant food

availability. Gosálbez and Castién (1995) investigated the above parameters of *A. flavicollis*, during two years differing in forest seed production and showed that the amount of available food had an effect on the number of reproductive periods in females and on the level of testicular activity in males.

Our sample area was a *Querco robori-Carpinetum* forest habitat situated in South-Hungary, with *A. flavicollis* being a dominant component of the resident rodent community. Based on capture results in 1997, our aims have been to demographically analyse the *A. flavicollis* population found there and to test for a possible effect of age on survival.

Material and methods

Our study area is located between the villages Vajszló and Páprád (N 45° 51', E 18° 00') in county Baranya, on the Dráva Lowlands. The 1-ha sampling quadrat was set up in a hornbeam-oak (*Querco robori-Carpinetum*) forest section, where the height of the upper canopy was around 25 m, with the characteristic species being *Quercus robur, Fraxinus angustifolia* and *Robinia pseudoacacia*. The lower canopy layer was 4-10 m high where *Carpinus betulus, Ulmus minor, Fraxinus angustifolia* were characteristic. The shrub layer of 1-4 m height consisted of *Cornus sanguinea, Ligustrum vulgare, Crategus monogyna, Sambucus nigra* and young specimens of *Robinia pseudoacacia*. Patches of the area with high undergrowth of 90-100 % cover were characterised by species indicating nitrogen-rich habitats.

The sampling quadrat was oriented approximately along the northeast-southwest geographic axis. The grid covered one hectare with 11 by 11 box-type live traps at an equal distance of 10 m from each other. Bacon and whole cereals were used as bait. Data from 10 months in 1997 were processed. Five-night sampling sessions were repeated monthly from February to November 1997, yielding 6050 trap nights. Traps were checked twice daily (8^{00} CET and 20^{00} CET). For individual identification of the animals the removal of the first knuckle of toes (O'Farell 1980, Nichols and Conley 1982) was used, and the following data were recorded: species, sex (in females gravidity or lactation too), age and weight. Age was determined based on external features and weight, with the help of the study by Haferkorn and Stubbe (1994). The computer program JOLLYAGE (Hines 1988) was used for testing age-dependent survival models and to estimate survival and population size.

For age dependent modelling the following conditions are required: all individuals of a particular age group (v) have equal capture probability ($p_i^{(v)}$), if the individual is present alive in the population at the time of the i^{th} sampling (i=1, 2,...,k) (1); all marked individuals of a particular age group (v) have equal survival probability ($\Phi_i^{(v)}$) during the trapping period between i and (i+1), if the individual is present alive in the population at the time of the i^{th} sampling (i=1, 2,...,k) (2); no markings are lost during the study and all are correctly identified upon capture (3); emigration is constant (4); the age of each individual is identified correctly (5).

Before the estimations are done, it is essential that possible ratios of survival and capture rates of the various age groups can be tested for. This can be done, as Pollock (1981) indicated, by using a series of chi-tests relying on proper statistical data. The program JOLLYAGE uses a model assuming three constant survival and capture probabilities. These models use a limited number of parameters which results in a high accuracy of estimated values, because the number of estimations is smaller. They simplest reduced-parameter, age-dependent models apply two age-groups (0 and 1, or juvenile and adult), and assume that the time necessary for individuals to enter adult category from the juvenile one equals the time between the samplings (usually 1 year). Brownie *et al.* (1986) developed two such models, which are the generalized versions of Models B and D calculated by the JOLLY program (Hines 1988) applying the Jolly-Seber estimator for open populations, where juvenile and adult animals are marked in each period. Following the terminology of the JOLLY program, we refer to these as Models B2 and D2. These models, with Pollock's (1981) age-dependent model added, are the following:

In model A2, or the generalized Pollock Jolly-Seber model l = 1; and the model assumes a time-dependent survival rate for both juveniles and adults ($\phi_i(0)$), and ($\phi_i(1)$), and a time-dependent adult capture probability (p_i (1)).

Model B2 assumes constant survival rate for both juveniles and adults (ϕ_i (0) = ϕ (0), ϕ_i (1) = ϕ (1), i = 1,..., k-1), and time-dependent capture probability (p_i (1)).

Model D2 assumes constant survival rate for both juveniles and adults (ϕ_i (0) = ϕ (0) , ϕ_i (1) = ϕ (1) , i=1,..., k-1) and constant capture probability (p_i (1) = p (1), i = 2, ..., k).

The detailed description of estimations and tests applied in model selection is presented by Brownie *et al.* (1986), and its supplemented version, for developing computer algorythms, appears in Brownie (1985). These algorythms were combined and were incorporated in the JOLLAGE program, which (in

addition to analyses described above) also provides estimation for B2 and D2 models, "goodness of fit-tests", and homogeneity tests among models (χ^2-test).

All three models of the program were applied and tested with capture data of *A. flavicollis* (Pollock *et al.* 1990).

From the standard error of estimated population size (N_i), the relative accurateness of the estimation, i.e. the variation coefficient of N ($cv(N)$) was calculated (White *et al.* 1982).

Results

During the 6050 trap nights, 306 *A. flavicollis* individuals were marked. Both our capture results and the JOLLYAGE output parameters showed that the number of adult specimens was higher than that of juveniles (Table 1). The appearance of a relatively large number of juvenile specimens occurred in June, since the reproductive period reached its peak around the end of spring. There were no young individuals in the last two (autumn) study months.

Table 1. Capture parameters under the output of JOLLYAGE for *A. flavicollis*

Sampling period	m_i	n_i		R_i		r_i		z_i
	Adult	Adult	Juv.	Adult	Juv.	Adult	Juv.	
February	0	18	0	18	0	15	0	0
March	11	21	0	21	0	13	0	4
April	11	19	3	19	3	11	0	6
May	12	35	9	35	8	22	0	5
June	20	35	25	35	24	19	4	7
July	19	32	1	32	1	14	0	11
August	18	53	8	53	8	26	1	7
September	27	68	8	65	8	37	0	7
October	41	56	0	51	0	27	0	3
November	30	39	0	38	0	0	0	0

m_i : is the number of marked individuals caught in sample i
n_i : is the total number caught in sample i
R_i : is the number in the ith release
r_i: is the the number of the R_i that are subsequently recaptured
z_i: is the number of marked individuals present at the time of sample i, not caught in sample i, but subsequently recaptured

The age-dependence of survival probability and capture probability was proved by the significant χ^2 values of the 2×2 contingency tables, in four sampling occasions. The test on the entire sampling period also supports the age-dependence of the two probability parameters (Table 2).

JOLLYAGE tests the capture parameters of the two age-groups with a series of goodness-of-fit ('GOF' that is) tests, in two steps (in accordance with capture histories): with a 2×3 and a 2×4 contingency table, using which it compares the capture rates of each age group. Our data of the 2×3 contingency table were homogenous with the theoretical values in all of the periods and, of course, in the total χ^2 value as well ($\chi^2 = 9.17$, $P = 0.327$). In the case of the 2×4 table the test did not work in all of the periods, but eventually it showed homogeneity between our data and the theoretical values ($\chi^2 = 9.17$, $P = 0.327$). The results of the goodness-of-fit test comparing the three models are shown in Table 3.

Table 2. Contingency chi-square test for age-dependent survival and capture probabilities

Sampling periods (i)	Contingency table		Test statistics		
	$r_i^{(0)}$	$R_i^{(0)} - r_i^{(0)}$			
	$r_i^{(1)}$	$R_i^{(1)} - r_i^{(1)}$	χ^2	df	P
5. (June)	22	0	10.29	1	0.0013
	13	8			
6. (July)	19	4	8.47	1	0.0036
	16	20			
8. (September)	26	1	3.76	1	0.0523
	27	7			
9. (October)	37	0	9.23	1	0.0024
	28	8			
Overall test statistics			31.77	4	< 0.001

$R_i^{(0)}$: the number of juvenile individuals released after the ith sample
$R_i^{(1)}$: the number of adult individuals released after the ith sample
$r_i^{(0)}$: the number of the $R_i^{(0)}$ that are captured again at least once after the ith sample
$r_i^{(1)}$: the number of the $R_i^{(1)}$ that are captured again at least once after the ith sample

The goodness-of-fit test of model A2 shows that the age-dependent A2 model fit the data, implying that the group of age-dependent models is appropriate for the data of *A. flavicollis*. The test did not reject models B2 and D2 either, therefore it is concluded that all three models fit the data. When the models were compared, model A2 did not reject the simpler model D2, while in the pair B2 vs. A2 a difference with 10% error was found between the two, suggesting that at this low level of significance A2 rejected model B2 which is simplified in its survival estimation. Accordingly, both A2 and D2, the latter using constant capture and survival probability, were appropriate for the analysis of the sample *A. flavicollis* population.

The age-specific survival estimates of models B2 and D2 were more accurate than the age- and time-dependent estimates of A2. The survival values of model D2, especially those calculated for adults, are close to the mean values of A2. The test between models B2 and D2 is not valid, and it was shown that model A2 rejected B2, whereas it did not reject D2. Consequently, among the age-dependent reduced-parameter models, it is the simpler D2 model fitting our data that appeared more applicable in analysing the population of *A. flavicollis*.

Table 3. Results of goodness-of-fit tests and tests comparing models for *A. flavicollis*

	Goodness-of-fit test				Test between models		
Model	χ^2	df	*P*	Models	χ^2	df	*P*
A2	13.26	11	0.2764	B2 vs. A2	12.33	7	0.0899
B2	25.6	18	0.1092	D2 vs. B2	8.89	8	0.3516
D2	33.23	26	0.1556	D2 vs. A2	19.96	15	0.1734

Based on the above findings of model selection, results of model D are shown: the numbers of marked individuals in the trapping periods appear in Fig. 1. There are two maxima in the demographic trend of *A. flavicollis* in 1997, based on the estimated number of marked animals. The first peak in July drops back by August, and the second maximum in the proportion of marked individuals occurs in autumn.

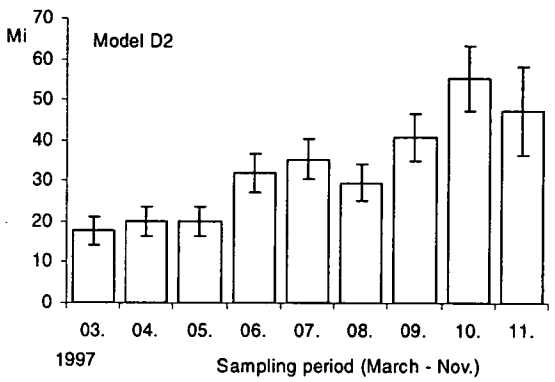

Fig. 1. Estimated numbers of marked individuals in the sampling periods for *A. flavicollis* (with 95% confidence intervals also indicated).

The population size estimates calculated using model D do not show the bimodality in the number of marked individuals, which is a consequence of the higher number of recaptures (Fig. 2). The peak of *A. flavicollis* numbers occurred in September (ND2 = 105.07).

The relative accurateness of population size was tested by calculating the coefficient of variance (Fig. 3). Values of model D2 are well below 20 %, which means that the estimated values of population size are acceptable.

Model A2 of the program JOLLYAGE calculates survival rates of both adults and juveniles, and the capture rates of adult animals for each period. Model B2 operates with a constant survival rate in both age groups, while it calculates adult capture rates for each period. Model D2 gives a constant survival rate for both age groups and a constant value for capture probability of adults. Survival rates are given for all models (Table 4). Adult and juvenile survival rates were compared using t-test, which revealed that model A2 produced significantly higher survival rates of adult individuals (t = 11.41, P < 0.001). Similarly, the combined results of models B2 and D2 showed that adult survival rate was the higher.

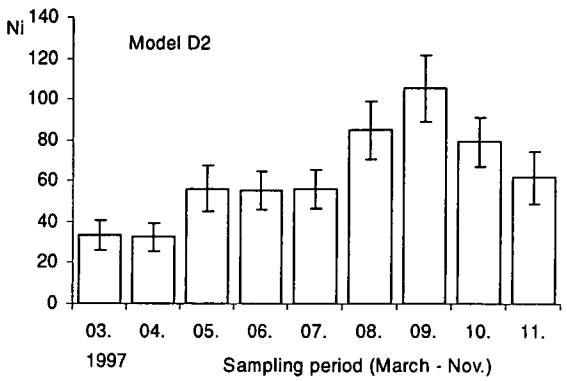

Fig. 2. Estimated population size under the Model D2 of JOLLYAGE for *A. flavicollis* (with 95% confidence intervals also indicated)

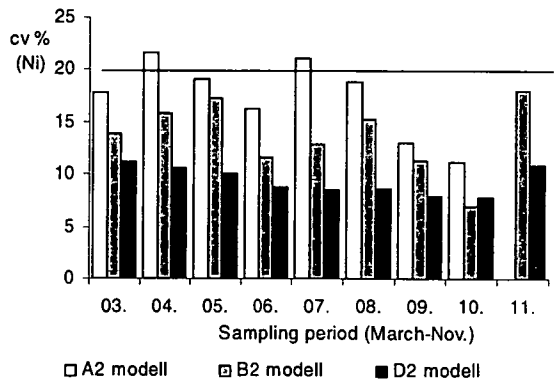

Fig. 3. Coefficient of variation of the population size estimators (A2, B2 and D2 model)

Survival rates calculated by model A2 decreased as numbers of *A. flavicollis* grew (Fig. 4). However, the number of sampling months was not sufficient to prove the negative correlation between the number of marked individuals and survival rates, therefore this relationship cannot be considered to be significant. The effect of density, despite the lack of significance in the correlation, should be viewed as an important factor, in addition to age.

Table 4. The survival and capture rates of *A. flavicollis* under the models of JOLLYAGE

Model	Sampling period	Adult survival rates $\phi_i^{(1)}$ (S.E.)	Juvenile survival rates $\phi_i^{(0)}$ (S.E.)	Adult capture rates $p_i^{(1)}$ (S.E.)
A2	1. (February)	0.96 (0.13)	* (*)	
	2. (March)	0.76 (0.16)	* (*)	0.64 (0.14)
	3. (April)	0.68 (0.14)	-	0.52 (0.14)
	4. (May)	0.76 (0.12)	-	0.61 (0.13)
	5. (June)	0.78 (0.16)	0.24 (0.11)	0.61 (0.11)
	6. (July)	0.56 (0.12)	-	0.44 (0.11)
	7. (August)	0.57 (0.09)	0.14 (0.13)	0.56 (0.11)
	8. (September)	0.60 (0.07)	-	0.69 (0.09)
	9. (October)			0.88 (0.06)
	Mean	0.71 (0.03)	0.06 (-)	0.62 (0.04)
B2	2. (March)			0.70 (0.12)
	3. (April)			0.57 (0.12)
	4. (May)			0.61 (0.12)
	5. (June)			0.64 (0.10)
	6. (July)			0.52 (0.09)
	7. (August)			0.57 (0.10)
	8. (September)			0.65 (0.09)
	9. (October)			0.83 (0.08)
	10. (November)			0.76 (0.11)
	Overall	0.67 (0.03)	0.12 (0.05)	0.65 (0.11)
D2	Overall	0.69 (0.03)	0.11 (0.05)	0.64 (0.04)

* Mathematically unvalid

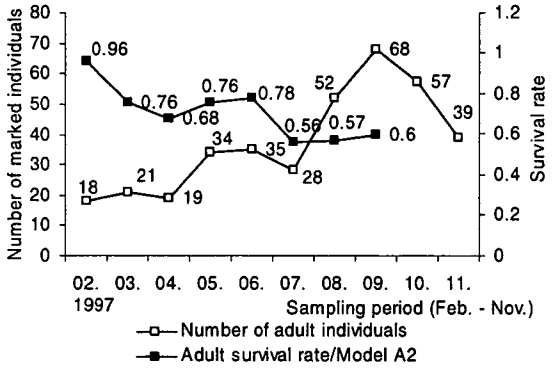

Fig. 4. Number of adult individuals and survival rate in different sampling periods

Discussion

The GOF-analysis of *A. flavicollis* capture data showed that the application of age-dependent model-groups of the programme JOLLYAGE was reasonable, since we proved the age-dependence of survival- and capture probability, the testing of which was thought to be important also by Pollock *et al.* (1990). The capture parameters of *A. flavicollis* were adequate for the condition system of the model, with the GOF-tests yielding homogeneity for all three models. Following Lebreton *et al.* (1992) we first analysed the application of the global model in our model selection, then, based on the homogeneity tests between the models, we chose the simplest, reduced-parameter model. Besides the reduced-parameter D2 model, the global A2 model also appeared appropriate, yet based on the above finding we decided to rely on the estimated values of the simpler D2 model. In the case studies cited by Pollock *et al.* (1990) the probability of the loss of a certain proportion of the individual markers was mentioned as a factor likely to distort JOLLYAGE results. In our case when *A. flavicollis* individuals were toe-clipped, marking was permanent, thus the possibility of the loss of the marker could be exluded.

In the annual cycle of *A. flavicollis* population dynamics, abundance maxima usually occur between August and October (Flowedew 1985). Jensen (1975), however, recorded that peak density in a beech forest occurred later, in November. The results of this study confirm the former period, since the maximum value of estimated population size was obtained for September. The subsequent drop in numbers is remarkably influenced by the amount of available food. In cases when food is abundant in the habitat and there is winter reproduction, population size can grow even through the winter (Bobek 1973). Although in our study we analysed only one period, there is evidence from earlier studies for big differences between annual peaks, which, again, is

related with food availability and the length of the breeding period (Adamczewska 1961, Hoffmeyer and Hansson 1974, Montgomery 1980).

Our estimated survival rates, obtained within a one-year period, decreased as population density grew. This negative correlation was not significant but was in accordance with similar findings by Bobek (1973) for the same species. The growth of density raises the question of how the spatial organisation and the age-structure of the population, and the dynamics of immigration and emigration change. There is relatively little information about the spatial organisation and movement patterns of *A. flavicollis* (Wolton and Flowerdew 1985). We can assume that as density grows, space utilisation also increases, which will, beyond a certain degree of food source decrease, lead to increasing emigration. At the same time, appropriate food availability for individuals within the habitat, together with intraspecific relations within the population and territoriality in home ranges will restrict the number of recruitment individuals. Accordingly, survival as estimated from capture-recapture will also decrease, thus is density-dependent. When studying mainly the spatial relations and behaviour, Mazurkiewicz and Rajszka-Jurgiel (1988) attributed primary role to food source in the forming of density. Their analysis of emigration and immigration showed that considerable dispersion in search for food occurred at low levels of density, which finding appears to contradict the above assumption. Their case study, however, did not include estimations and compare-isons of survival which has prime importance in the density-dependent explanation of spatial and temporal patterns of populations.

Obviously, a longer trapping period would have provided more data for proving the density-dependence of survival. However, within the same habitat, enormous differences between population sizes of the years could have resulted from variations in the amount of available food and changes in intra- and interspecific relations, which can greatly influence values of survival estimated from capture-mark-recapture data, and can thus considerably distort statistics that could prove the density dependence of survival.

Acknowledgments

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TISCIA 34, 41-46

EFFECT OF DENSITIES OF TWO COEXISTENT SMALL MAMMAL POPULATIONS ON THE SURVIVAL OF *APODEMUS FLAVICOLLIS* IN A FOREST HABITAT

Gy. Horváth and Z. Wagner

Horváth, Gy. and Wagner, Z. (2003): Effect of densities of two coexistent small mammal populations on the survival of *Apodemus flavicollis* in a forest habitat. — *TISCIA 34, 41-46.*

Abstract. Small mammal populations were observed by live-trapping in a forest reserve area of *Querco robori-Carpinetum* plant association on the Dráva Lowlands in southern Hungary in 1997. During the 6050 trap-nights resulting from the 5-night sampling periods, 306 individuals of *Apodemus flavicollis*, 269 of *A. agrarius* and 293 of *Clethrionomys glareolus* were captured and marked. The comparative analysis of population dynamics showed that synchronous changes in the number of individuals occurred only in the case of *C. glareolus* and *A. agrarius*, while in the other two pairings these changes advanced without any similarities. The interaction matrix which was constructed based on the calculated partial regression coefficient, indicated negative interaction relation among the three species. The present study investigates whether the densities of the two coexistent populations have an effect on the survival of *A. flavicollis*. The hypothesis was analysed with the program MARK. A constrained-parameter model was designed and our assumption was proved: according to the model selection procedure the survival of *A. flavicollis* is influenced by the two coexistent populations. In further analyses the values of estimated survival probabilities were compared and as a result no consistent difference could be indicated between the survival probabilities calculated by the derived CJS and the constrained parameter models. Thus, the influence of the two coexistent populations is not so notable that it could cause significant differences.

Key words: Apodemus flavicollis, survival, constrain parameter, model selection

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Introduction

The typical generalist species in Central-European deciduous forest area are the yellow-necked wood mouse, *Apodemus flavicollis* (Melchior 1834), the bank vole, *Clethrionomys glareolus* (Schreber, 1780) and the striped field mouse, *Apodemus agrarius* (Pallas, 1771). Their habitat preferences differ only to a little extent. *A. flavicollis* and *C. glareolus* are characteristic forest dwellers (Flowerdew *et al.* 1985, Mazurkiewicz 1994), while *A. agrarius* can be found in fields, agricultural areas, yards and wet, bushy habitats, along rivers and in forest edges, forest stripes (Zejda 1967, Pucek 1983, Szacki and Liro 1991).

The trophic niches of the three species are very similar, the pattern of their spatial distributions are comparable, though the food resources in the different habitats and seasons can adequately be differentiated (Holisova 1967, Obrtel and Holisova 1974, Hansson 1985). If the three species are either temporarily or permanently present in a given habitat, competition relations can evolve. Several studies have been published on the analysis of the different interspecific interactions of these species. Andrzejewski and Olszewski (1963) investigated the direct competition of *A. flavicollis* and *C. glareolus*. They also observed the daily activity of the two species, on which the fluctuation of their densities is of great influence. At high density the activity of *C. glareolus* decreased, when the *A. flavicollis* was at its

activity peak (Wojczik and Wolk 1985). With respect to *A. flavicollis* and *C. glareolus* the selective removal of the former caused an increase in the number of *C. glareolus* adult females in the area (Bujalska and Janion 1981). It was proved that *C. glareolus* had a constraining effect on the density and spatial distribution of *A. agrarius*, although the relationship between the two species is highly influenced by the qualitative characteristics of the given habitat (Kozakiewicz *et al.* 1987). Based on the evaluation of density values, Gliwicz (1981) indicated negative associations between *A. flavicollis* - *A. agrarius* and *C. glareolus* - *A. agrarius*, and suggested significant overlap between the food resources as the cause for competition in the case of the two pairings but he also mentioned competition for hiding places as an alternative hypothesis. Kozakiewicz and Boniecki (1994) studied the inter- and intraspecific behaviour of *C. glareolus* and *A. agrarius*, and they reported that intolerant relations are likely to evolve between them, which are as strong as the agonistic relations within the species. However, these experiments did not prove the earlier statements that the *Apodemus* genus is dominant over *Cletrionomys* (Gurnell 1985).

Applying the density values of three earlier years in the present study area, an interaction matrix was constructed based on the calculated partial regression coefficient and in the case of all three pairings of the three populations strong negative interactions were pointed out (Horváth *et al.* 1996). 1997 was a very high-density year regarding all three populations. According to our assumption, the interactions among the three species have great influence on the density of each given population and the changes in it have effects on the survival of the individuals. The present study observes the hypothesis whether the densities of *C. glareolus* and *A. agrarius* higher than their average density in each period have constraining effect on the survival and recapture probabilities of *A. flavicollis* based on the data from 1997. The purpose of the analysis is to find out if the negative interaction shown by the interaction matrix could also be proved by modelling the survival, thus the densities of the two coexistent populations have justifiable constraining effect on the survival of *A. flavicollis*.

Materials and methods

Our study area is located between the villages Vajszló and Páprád (N 45° 51', E 18° 00') in Baranya county, in the Dráva Lowlands of Southern Hungary. The trapping grid covering 1-ha area was laid out in a hornbeam-oak (*Querco robori-Carpinetum*) forest section where the height of the upper canopy is around 25 m, and the characteristic species are *Quercus robur, Fraxinus angustifolia* and *Robinia pseudoacacia*. The lower canopy layer is 4-10 m high, where *Carpinus betulus, Ulmus minor, Fraxinus angustifolia* are the typical representatives of plants. The shrub layer of 1-4 m height consists of young individuals of *Cornus sanguinea, Ligustrum vulgare, Crategus monogyna, Sambucus nigra and Robinia pseudoacacia*. Sections of the sampling area with the densest plant cover of 90-100 % are characterised by high undergrowth comprising many weed species and ones indicating dampness and soil rich in nitrogen.

The area was oriented approximately to northeast-southwest with 11×11 live traps positioned 10 m apart from each other. Mixed cereals and bacon were used as bait. Data from 10 months of 1997 were used in the research. Sampling with five-day trapping sessions each month from February to November made up 6050 trap nights. Traps were checked twice daily (8^{00} CET and 20^{00} CET). We marked the individuals by removing the terminal knuckle of certain toes (O'Farell 1980, Nichols and Conley 1982). The temporal changes of population sizes in the three observed species were characterized by "minimum number alive" (MNA) (Krebs 1966, Boonstra and Krebs 1978). Based on the MNA-values the trends in the numbers of individuals were compared and evaluated with Spearman rank-correlation (Zar 1996). Interaction matrices were constructed using the demographic data and calculating the partial regression coefficient (Dueser and Hallett 1980).

The analysis of time-dependence in the survival and recapture rates of *A. flavicollis* was carried out with the program MARK (Cooch and White 1998). The model chosen by the goodness-of-fit (GOF) tests was held as the basic model and it was compared to the constrained parameter model, where the effect of densities of *C. glareolus* and *A. agrarius* was built in the model-matrix using the applications of the program MARK. Constraining effects were considered in those periods where the densities of *C. glareolus* and *A. agrarius* were higher than that of the *A. flavicollis* population. The constrained parameter model-matrix also allows to take the conjugate effects of densities into account. The model selection between the basic and the constrained parameter models was based on the differences in the models' deviances and the values of AIC (Akaike Information Criterion) calculated by MARK (Anderson *et al.* 1994). The latter handles not only the model-bias from our data, but also the number of parameters (PAR) that influences the

accuracy of the estimates [AIC = Dev. + 2 × PAR]. The survival rates estimated by the models were compared using the one-sample *t*-test.

Results

During the 6050 trap nights 306 specimens of yellow-necked wood mice (*Apodemus flavicollis*), 269 striped field mice (*A. agrarius*) and 293 bank voles (*Clethrionomis glareolus*) were captured and marked. The demographic trends of the rodent populations throughout the 10-month sampling period were evaluated based on the changes in the MNA values (Fig. 1). Two abundance maxima can be observed in both *A. flavicollis* and *C. glareolus* which do not coincide in the two species. The former had its maximum in May-June and later in September, while the latter was the most abundant in July and October. *A. agrarius* was captured in low numbers in February-March, suggesting low overwintering survival in the high-density autumn population, according to the numbers of captures. Thereafter, similarly to earlier years, the density of *A. agrarius* decreased over the summer period but in autumn it showed intensive increase again and by September its MNA value outnumbered those of the other two species. The intensive increase in the density of this species raises the question how this high density evolving in such short a period would effect the actual number of the two coexistent populations. The decline in the population sizes after the autumn period in the case of all three species indicates the reduction in resources and the beginning of the lower-density winter period.

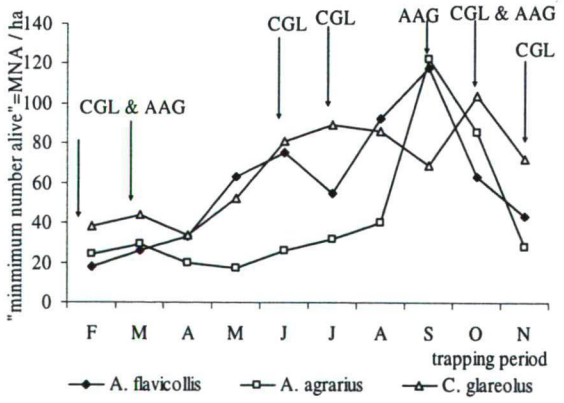

Fig. 1. Demographic changes in the three rodent populations. Sampling occasions where the density of *C. glareolus* or *A. agrarius* or of both was higher than that of *A. flavicollis* were indicated with arrows.

As revealed by the comparative analysis of population dynamics during the sampling year, the demographic trends of *C. glareolus* and *A. agrarius* showed significant synchronous changes ($R_S = 0.636$, $p < 0.05$), while no rank-correlation values were obtained in the population shifts in the other two pairings (R_S = 0.516 - 0.565, NS). The interaction matrix based on the calculation of partial regression coefficient from the demographic data indicated negative relation among the three species (Table 1).

Table 1. Interction matrix for captured rodent species based on the partial regression coefficients

Species	*A. flavicollis*	*A. agrarius*	*C. glareolus*
A. flavicollis	-		
A. agrarius	r = - 0.9929 *	-	
C. glareolus	r = - 0.9916 *	r = - 0.9919 *	-

*: p < 0.001

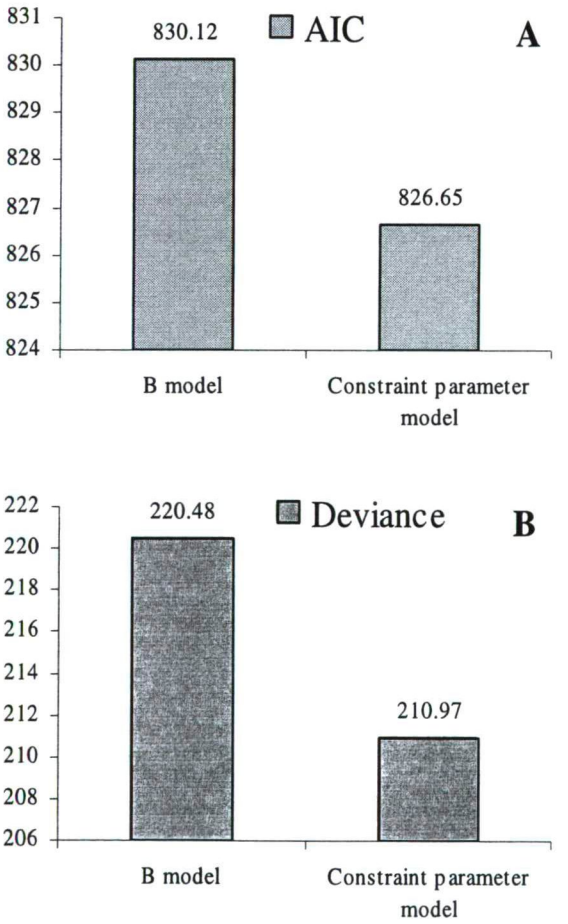

Fig. 2. The values of AIC (A) and deviances (B) by fitting the data of *A. flavicollis* on the B and the constraint parameter model.

The two statistical analyses above suggest a competition relation among the three coexistent populations, therefore our assumption was that on

any of the three populations the density of the other two had a constraining effect, which has influence on the survival probability of the given population. Thus, survival models were carried out further on.

First, the time-dependence of survival and recapture probabilities of *A. flavicollis* were tested based on the capture history of the individuals in the population. According to the GOF-test of MARK, the B model [ϕ (t), p()] assuming time-dependent survival through the sampling periods derived from the basic CJS model was accepted as the most parsimonious model ($\chi^2 = 0.645$, $df = 6$, $p = 0.9956$). The constrained parameter model was compared to this one. The density of *A. flavicollis* was in six periods lower than that of *C. glareolus*, in four periods lower than *A. agrarius* and in three periods both of the two coexistent populations exceeded the density of the observed population (Fig. 1). The estimated deviance for the constrained parameter model that could handle, in addition to their individual effect, the conjugated effect of the two coexistent populations on *A. flavicollis*, was lower than the basic model, assuming survival to be time-dependent ($\chi^2 = 9.52$, $df = 1$, $p < 0.01$). Besides, considering the AIC values it was again the constraint parameter model that fitted our data better (Fig. 2). The results of model-selection proved our hypothesis assuming the density of *A. agrarius* and *C. glareolus* to be a constraining factor, which therefore could have negative influence on the periodically estimated survival probabilities of *A. flavicollis*. The density of *A. agrarius* and *C. glareolus* plays a role in the survival of *A. flavicollis* as a biotic factor.

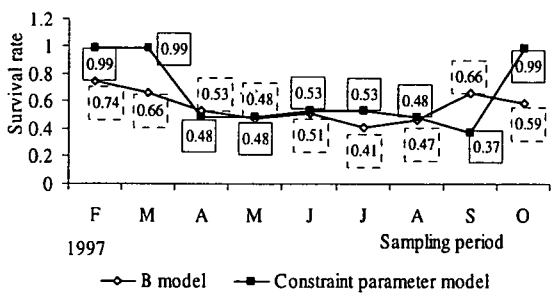

Fig. 3. The estimated survival rates of *A. flavicollis* population.

The survival probabilities estimated by the basic and the constrained parameter models are shown in Fig. 3. Based on the results of model-selection the survival values estimated by the constraint parameter model were expected to be lower in those periods when the two other populations were present as constraining factors. In several periods marked differences occurred: in two months (April, September) the survival probabilities were lower than those estimated by the basic model, however in three other months (February, March, October) they were higher. Thus, Fig. 2 directly shows that the survival probabilities of *A. flavicollis* were not reduced significantly by the densities of the two coexistent populations. Despite of the result of the model selection these parameters did not change according to our expectance. As a further analysis, t-test was administered between the survival probabilities estimated by the two different models and there was no significant difference between them ($t = 0.77$, $df = 8$, NS).

Based on the model-selection carried out by MARK, the constrained parameter model was accepted as the most adequate for simulating the population dynamics of *A. flavicollis*, according to which the two persistent populations have real effect on its survival probability. However, this effect was not so notable to cause statistically significant differences between the values. Of course the interaction among populations is one factor from the numerous background variables in charge of the changes in survival probability. As shown in the present experimental study the fluctuation in density and its effect was not as great as it was assumed by the interaction matrix constructed on the basis of demographic changes in the populations.

Discussion

Research has been carried out in the forested study area since 1994. Regarding the changes in population dynamics, the sampling data of 1997 i.e. the fourth year of experiment proved earlier observations. This study year yielded much higher captures which was not only a result of the modification of sampling procedures but also an aftermath of favourable weather (mild winter and better spring conditions for the overwintered individuals as an initial generation). According to earlier studies if *A. flavicollis* reaches a demographic peak, it will show aggression against other species (Hoffmeyer 1973), though in grassland area it only passively effects the dispersion of the coexistent populations. The negative interaction could be a result of aggression evolving in the reproductive period (Sadleir 1965). Hansson (1971) claims that the negative relation between *A. flavicollis* and *C. glareolus* evolves because of their demand for similar food supply. In 1997, beside *A. flavicollis* the number of individuals of *C. glareolus* increased to a great extent. Ylönen and Viitala (1991) also observed the decrease in the densities of the two

species over the winter period as it was shown in the present study, and they declared that the two most important factors in population distribution are the availability of food supplies and the patchiness of the area. The growth in number of individuals justifies the statement of Grant (1974), where he claims that there is a 3-4-year periodicity in the demographic peaks of *C. glareolus*, which was also reflected in our earlier observations.

Having carried out researches on interactions between populations, Gliwicz (1988) investigated *A. flavicollis* and *C. glareolus* using the removal method, during which she reported two dispersion periods: in spring - early summer and in autumn. The rate of dispersion and the rate of population growth are in correlation, and their correlation is effected by the presence of reproductive periods. Social mechanisms depend highly on the habitat and its structure, on food supply and the animal's space of life, i.e. its residence resulting from its behavior and search strategies. Each population showed two peaks during the one-year experiment, which is in accordance with the idea of more dispersion waves pointed out by Gliwicz (1988). The periods of peaks recorded in our sampling area are identical with those observed in Poland. The Spearman rank correlation indicated synchrony between the demographic trends of *A. agrarius* and *C. glareolus*. However, the interaction matrix based on the calculated partial correlation coefficient proved the existence of the assumed negative interaction between them. It has already been pointed out in our earlier studies that the negative partial regression value suggests competition relation (Horváth *et al.* 1996). Their interaction with respect to competition was discussed by Gliwicz (1981) in details, she indicated the negative relation between the two populations by calculating the Cole association coefficient. The interaction matrix based on her data is identical with the results of Polish researcher. Flowerdew (1985) observed the demographic dynamics of *A. flavicollis* and he noted that its reproduction is effected by the density, the food supply and the climatic factors, but in the reproduction period (Feb/Mar – Oct), the population growth is not disturbed by the lack of recruits. The reproduction period of *A. flavicollis* begins in spring, peaks in autumn and decreases in winter, but its survival remains sufficient throughout the whole year. The over-reproduction in the autumn-winter period is suppressed by the density-dependent reproduction and dispersion of *A. flavicollis* females. In cases of abundant acorn yield and after probable winter mating the population number increases.

Considering the above mentioned competition relation, the survival of *A. flavicollis* was analysed assuming the constraining effect of the two coexistent populations. According to the model selection procedure we could prove the effect of the two coexistent populations but the survival probabilities estimated by the models did not differ significantly. The hypothesis that the constraining effect of density decreases the estimated values of survival could not be proved in every sampling period. A long-term observational period with extended data from several years could provide more precise results that would support our hypothesis more adequately. Among the background effects, the density of coexistent populations is only one factor that has influence on survival rate. Several biotic and abiotic factors should also be examined when the changes in survival are to be appropriately interpreted.

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TISCIA 34, 47-56

SPECIES TURNOVER AS A FUNCTION OF VEGETATION PATTERN

K. Virágh and S. Bartha

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Abstract. In Hungary, during the secondary succession after deforestation xeromesophilous *Brachypodium pinnatum* community often develops and gradually turns into xerophilous grassland. This study reports on fine-scale plant species turnover in three types (Forest-type, Forest-steppe- and Steppe-types) of *Brachypodium pinnatum* dominated grassland, representing constrasting stages of steppe formation. Micro-maps of rooting individuals (or ramets) of vascular plant species were recorded in 20×110 grids of contiguous 5×5 cm microquadrats over three subsequent years. We found that local species turnover showed a slightly increasing tendency from forest to steppe types of *Brachypodium* grassland, coinciding with the declining dominance of *Brachypodium pinnatum* and the slightly increasing number of open spaces (gaps) for local plant colonization. Our results indicated that local species turnover patterns were temporally and spatially non-random in all *Brachypodium* grassland types. High and low local species turnovers were dependent on the spatial structure of vegetation. Spatial behaviors of some matrix-forming grass species proved to be important for structuring the fine-scale species turnover patterns. We found contrasting differences according to the abundances of species. Local turnovers were the lowest in the *Brachypodium pinnatum* dominated microquadrats of the Forest-type and similarly, in the Festuca rupicola dominated ones, but only in the Steppe-type. The highest turnovers were revealed in the *Bromus erectus* dominated microquadrats. *Brachypodium pinnatum* decelerated fine-scale turnovers in all types, as the relationship between pattern of presences of this species in the microquadrats and the spatial pattern of high local species turnovers was significantly negative. *Festuca rupicola* both accelerated and decelerated local turnovers, dependently from its coenological status. Spatial patterns of *Bromus erectus* and *Festuca rupicola* were not correlated only with the turnover patterns of Forest-steppe - type. It was stated that behaviour of key grass species in controlling the local species turnovers was not strictly specific but rather differed according to the various fine-scale vegetation patterns of grassland types.

Keywords: spatial associations, vegetation dependent local species turnover, key grass species, Brachypodium grassland

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Introduction

In current literature of vegetation dynamics, closely linked to the concept of patch dynamics, the studies of fine-scale dynamics, such as local species turnover and species mobility within a vegetation patch (stand) have been received great importance for understanding of both patterns of species coexistence, internal dynamics of plant communities and their consequences in community dynamics.

Considering the concepts and methods of fine-scale turnover approaches there exists a great variation. Temporal and spatial dynamics of individual species, usually referred to as mobility and species replacement (turnover), have been studied on fine-scale from the scale of 1 cm2 to 0.25 m^2 on

small permanent sub-plots, as well as on coarser scale from 1 m^2 to 25 m^2 plots within a community. These were measured as 1) year to year changes in species composition (Glenn and Collins 1990, 1992, Stampfli 1995, Hobbs and Mooney 1995, Tamás and Csontos 1998, Zhang and Skarpe 1995) and 2) cumulative species richness or frequencies (Klimes 1995, 1999, van der Maarel and Sykes 1993, 1997, Sykes *et al.* 1994, Partel and Zobel 1995, van der Maarel et al 1995, van der Maarel 1996a,b, GeiBelbrecht-Taferner *et al.* 1997) for assessment of community dynamics and as 3) species turnover on small plots within the community (Huber 1994, Otsus and Zobel 2002) or 4) in the form of species replacement diagrams (Thórhallsdóttir 1990, Herben *et al.* 1993). In the latter case spatial aspect of this mobility was shown in distribution maps of species and species mobility was combined with capacity for long-distance spreading, with phalanx and guerrilla plant strategies (Herben *et al.* 1993). A system of plant mobility types was proposed by van der Maarel (1996) and his carousel model set up in 1993 has been already discussed in various types of plant communities (Fröborg and Eriksson 1997, Maslov and van der Maarel 2000, del Moral 2000). Different measures of species mobility by indirect and direct indices have been recently summarized by Palmer and Rusch (2001).

As to the results on patterns of local species turnover and factors controlling their changes, it is not surprising, that there are various conclusions, depending on the structure and dynamical state of the studied vegetation and the scales of observation. For illustrating some contrasting opinions, few examples are mentioned.

Recently many studies of fine-scale plant mobility, performed in near-equilibrium or stable communities (van der Maarel and Sykes 1993, Rusch and van der Maarel 1992), have shown that the occupation of microhabitats proceeds at random within plots, where there is no dispersal limitation, and the degrees of colonization and extinction processes can be considered near the same in a year and are also consistent from year to year. On the contrary, several studies (Ryser 1993, van der Maarel *et al.* 1995) have concluded that spatio-temporal patterns of turnover within a community are not totally stochastic, mainly due to the great variation of local population densities, the limitation of seed dispersal and the growth forms and propagation strategies of plants. However, in spite of the fact that there have been increasing evidences on that majority of plant communities are spatially and temporally heterogeneous and fine-scale dynamics, such as local species turnover changes are constrained by the existing vegetation, there is a lack of studies considering the species turnover not only as a phenomenon but as a function of vegetation pattern.

In this paper, we present an analysis of fine-scale patterns of local plant species turnover in connection with spatial vegetation patterns of successional communities. We examine what differences appear in the fine-scale plant species turnovers of three stages of *Brachypodium* grassland and how they are influenced by the gap structure and vegetation canopy height and closure of a stand. In analyzing patterns of local species turnover in connection with spatial vegetation patterns, we only consider the patterns of high and low species turnovers. As previous fine-scale studies (Virágh and Bartha 1998a,c) revealed the differentiation of a characteristic species coalition for each of three patches of *Brachypodium* grassland and found three grass species, such as the mesic, shade- tolerant *Brachypodium pinnatum*, the shade-intolerant *Bromus erectus* and the light-demanding xeric *Festuca rupicola*, playing central roles in spatial organization and forming species coalitions, we expect that spatial patterns of these key grass species can control the patterns of local turnover. Thus, as a first step, we deduced vegetation pattern of a stand into patterns of these three matrix-forming species and to the patterns of turnover of subordinates.

The main objectives of this study are:

to analyze how local species turnover change in *Brachypodium* types with different species composition and spatial organization of species,

to compare the relative roles of some key grass species in controlling the patterns of local species turnover.

The following questions are examined:

are local species turnovers spatially and temporally dependent,

are local species turnover changes influenced by the species dominance structure and the canopy closure, and

are there any differences between the relative role of three key grass species according to controlling patterns of fine-scale species turnover and how are these differences related to the various fine-scale vegetation patterns of grassland types and the abundances and growth forms of these species.

Material and methods

Study site

Field studies were carried out in a landscape protection area in the central part of Hungary, 25 km east of Budapest, within a hilly landscape at 200-300

m a.s.l. Mean annual temperature of the site is 9 °C, mean January temperature is -1.5 °C, mean July temperature is +20.1 °C. Mean annual precipitation is about 600 mm distributed unevenly throughout the year. The most rainy seasons are late spring and early autumn with monthly precipitation maximum in May or June and the second lower maximum in October. Transitional soil types between brown forest soil and chernozem on loess substrate are typical here. The area was formerly covered by dry *Quercus pubescens* oakwood, which was clear-cut in the early 1900s (Anon. 1883, 1943). However, deforestation was incomplete and resulted in a heterogeneous mosaic of secondary successional habitats. The forest management activity stopped and the site had only occasionally been grazed since then. During a landscape-scale survey of the vegetation (Fekete *et al.* 1998) some remnants of oakwood, shrubland, and a patchwork of various xero-mesophilous grasslands on the northeast slopes were found.

Brachypodium pinnatum was the dominant component of the sparse undergrowth layer of the former dry oak woodland. Clones of *Brachypodium pinnatum* survived forest clear-felled and they developed into species rich xeromesophilous *Brachypodium* communities. These grasslands can persist for a long time and in certain conditions slowly change into a more xeric type of *Festuca rupicola* dominated grasslands. During these long-term changes many mesic, forest and forest-steppe species disappear, parallel with the colonization of several xeric loess steppe species.

Three typical vegetation types (Forest-type, Forest-steppe-, and Steppe-types) of *Brachypodium pinnatum* dominated grassland were selected for the present study. Most of the species are clonal perennials in these patches and annuals are scarce. The physiognomically uniform stands chosen are floristically and coenologically different from each other (Fekete *et al.* 1998) and each patch-type is spatially well-organized with complex multispecies coalition structures (Virágh and Bartha 1998a, Virágh *et al.* 2000).

Some textural attributes of three *Brachypodium* types are presented in Table 1. It is remarkable that few dominant and frequent (freq.: > 10%) and codominant and less frequent species (freq.: < 5%) occur in all patches, but the proportion of rare species (freq.: < 1%) is very high. Most of the species appear in the Forest-steppe type, but many codominant species are apparent in the Steppe-type.

Forest-type stands are dense and closed, where the average height of the sward is about 60-70 cm. A litter thickness is 10-15 cm. Numerous shade-tolerant species, remnants of the original forest vegetation live in a dense uniform canopy of *Brachypodium* clones, surviving under the shadow of scattered oak trees and *Crataegus monogyna* shrubs.

Table 1. Characteristics of three types of *Brachypodium pinnatum* grassland, 1993 (2200 microquadrats of 0.0025 m^2)

	Forest-type	Forest-steppe-type	Steppe-type
Total cover [%]	120	155	130
Average height of the sward [cm]	50-60	30-45	30-35
Litter thickness [cm]	10-15	5-10	2-6
Number of frequent species			
Frequency % > 10	3	5	6
Frequency % > 5	7	8	11
Frequency % > 1	16	26	22
Frequency % < 1	34	31	24
Number of abundant species			
Relative cover % > 1	9	13	16
Relative cover % < 1	41	44	30
Frequency %			
Brachypodium pinnatum	79.5	63.1	52.4
Festuca rupicola	23.7	17.6	20.3
Bromus erectus	5.9	24.7	25.8
Relative cover %			
Brachypodium pinnatum	74.9	35	22
Festuca rupicola	3.6	7.7	15.4
Bromus erectus	2.3	17.6	20

Forest-steppe-type is an intermediate stage from mesic communities to xeric ones. It contains a mixture of mesic and xeric species with many codominant dicots and broad-leaved grasses. The height of sward is 30-45 cm, the litter thickness is 5-10 cm.

Steppe-type develops after a long exposure to light and drought, as the result of invasion of xerophilous species. The viability and density of *Brachypodium* ramets are lower. The height of sward is 30-35 cm, and the litter thickness is only 2-6 cm here. The canopy is rather open, and the number of gaps is the highest in this patch.

These vegetation types also represent a light gradient associated with the declining dominance of *Brachypodium pinnatum* (Virágh and Bartha 1998a,b, Fekete *et al.* 2000, Fóti *et al.* 2002, Mojzes *et al.* 2003). There are three matrix grass species with different growth forms, such as the shade-tolerant *Brachypodium pinnatum* (a clone with sparsely distributed tillers), the shade-intolerant *Bromus erectus* of dense tussock and the drought tolerant, light demanding *Festuca rupicola* of sparse clump, which play important roles in coenological

differentiation at stand-scale and in spatial organization of species while forming characteristic multispecies coalitions at fine-scale. Their segregation in space is obvious in our communities, where they are generally significantly associated to the subordinated dicots and other grass species, but rare to each other (Virágh and Bartha 1998c).

Field sampling

Micro-maps of rooting individuals (or ramets) of vascular plant species were recorded in 20×110 grids of contiguous 5×5 cm micro-quadrats at the end of June, 1993, 1994 and 1995 in each vegetation type. Seedlings were not included, since they strongly differ in their resource use and competitive dynamics from the more established plants (Herben *et al.* 1993). Because of the heterogeneity and the limited size of the study area and the very laborious and time-consuming sampling, we could not sample many independent replicates of each vegetation type. However, when we studied the multispecies spatial patterns and interspecific associations in these three *Brachypodium* types (Virágh and Bartha 1998) and for a validation of the trends found we divided the 20×110 grids into two 10×110 subgrids and repeated the whole analyses with the pairs of subgrids, all trends remained the same showing the robustness of our results and indicating some stationarity of the studied vegetation patterns. Therefore, the analyses here concerned the whole 20×110 grids which could be also accept as representative for the *Brachypodium* stands.

Statistical methods

Species richness was measured at two different scales: microquadrat scale (the mean value per microquadrat) and stand scale (the total number of species found across all microquadrats within a stand, study area was 5.5 m^2). Colonization was expressed by the number of species appearing in all microquadrats (2200) of a stand in a year (t) but being absent in the previous (t-1) year. Similarly, extinction was calculated as the number of species disappearing from the microquadrats between two consecutive years. Relative colonization % was the ratio of the number of species appearing in all microquadrats in a year (t) and the total number of species present in that year (t). Relative extinction % was calculated as the number of species disappearing from all microquadrats of a stand between year (t-1) and year (t), divided by the number of species present in year (t-1) (cf. Gibson and Brown 1991, Bartha *et al.* 2003).

Fine-scale local species turnover (TO) was defined as the sum of the local (5×5 cm microquadrat scale) colonization and extinction between subsequent years. Note that the estimation of local turnover here was based on the numbers of newly appearing species and disappearing ones from each microquadrat between two consecutive years but could not consider the disappeared ramets which were replaced with new ones in the same microplots within a year. It means that in this sense local turnovers in our data may be underestimated. Percentage local relative turnover (*RTO%*) was calculated as $RTO\% = 100 \times TO/ST2$ where $ST2$ is the number of species in the micro-quadrats in the second year. Average local turnover and average local colonization and extinction were estimated at microquadrat-scale (the mean value per microquadrat). Because we were interested in the effect of dominant grasses (*Brachypodium pinnatum, Bromus erectus, Festuca rupicola*) on the turnover of all other (subordinate species), during the calculations of turnover values the three dominant grasses were omitted.

Percentage relative turnover data were transformed into binary data: $BRTO = 1$ if $RTO\% >$ the mean, and $BRTO = 0$ if $RTO\% <$ the mean, producing micro-maps with patterns of high and low local turnovers.

Micro-maps of species turnovers were analyzed by contagion indices, modified from indices used in landscape ecology (O'Neill *et al.* 1988, Li and Reynolds 1993).

$$Temporal\ contagion = \frac{1}{N}\sum_{i=1}^{N}\left(BRTO_{ij} - BRTO_{ik}\right)^2$$

that expresses the average temporal dependence of local species turnovers between subsequent years j and k. N is the number of micro-quadrats.

$$Spatial\ contagion = \frac{1}{N}\sum_{i=1}^{N}\left(\frac{1}{M_i}\sum_{n=1}^{M_i}\left(BRTO_i - BRTO_n\right)^2\right)$$

(M_i the number of proximate quadrats around microquadrat i, N is the number of micro-quadrats)

Because high and low turnovers could similarly appear in the adjacent quadrats by chance as well, we applied a null model, where the same local turnover values were used as in the field, however they were randomly assigned to the positions in the micro-maps (complete randomization from Diggle 1983). The observed values of contagion indices were compared with the values obtained from the null model. The significance was expressed as the relative frequency of the randomizations resulted in higher values than the observed one. 5000 randomizations were applied in each test. A significant result indicated the

tendency that the (spatially or temporally) adjacent micro-quadrats had similarly higher or lower species turnovers, i.e. the local species turnovers were not independent.

Relationship between species turnover and vegetation was investigated by calculating the spatial associations between the patterns of dominant grass species and the micro-maps of high/low local species turnovers.

From the basic grid data computerized sampling was performed with three different, increasing sampling unit sizes (5×5 cm, 5×10 cm, and 5×15 cm), and pairwise associations were calculated from 2×2 contingency tables:

$$mI\,(A,B)= m\log m+a\log a+b\log b+c\log c+d\log d-(a+c)\log(a+c)-(b+d)\log(b+d)-(a+b)\log(a+b)-(c+d)\log(c+d)$$

(Symbols *a*, *b*, *c*, and *d* correspond to the notation of the 2×2 contingency table. '*a*' is the number of sampling units where both variables, *A* and *B* are present, '*d*' is the number of empty quadrats. '*b*' and '*c*' note the number of quadrats, where only one variable is present, *A* or *B* respectively. $m=a+b=c+d$ is the sample size.)

Significance of any observed *mI* (*A,B*) value was calculated by comparing it with the values obtained by Monte-Carlo randomizations, i.e. representations of the null hypotheses. We used a null model where the presences of a variable were randomly redistributed among the quadrats, by using Monte-Carlo simulation (Site-model, Watkins and Wilson 1992). The significance was expressed as the relative frequency of the randomizations resulted in higher values than the observed one. 5000 randomizations were applied in each test. The trend of the association, i.e. whether the association was positive or negative, was given by a comparison of the expected and observed values of the joint occurrence of variables *A* and *B*. Calculations were repeated at three sampling unit sizes (5×5 cm, 5×10 cm, and 5×15 cm) at fine scales.

Results

Species turnover

The total number of species recorded in the 2200 microquadrats (5.5 m^2) ranged between 50 and 67 in the *Brachypodium* grassland types over 3 years (Table 2). Species richness was the lowest in the Forest-type and the highest in the Forest-steppe - type. Most of the newly detected species appeared in each vegetation type in 1994 and 1995. The average number of species of 0.0025 m^2 microquadrats ranged between 1.07 and 2.05 with a minimum of 0 and maximum of 8 species (Table 2). The percentage number of 5×5 cm vegetation-free gaps (species number is nil) varied between 4%-10% within a stand over 3 years, showing higher values in all grassland types in 1993 and lower values in two subsequent years. The number of gaps was slightly increasing from the mesic Forest-type to the xeric Steppe-type in each year (Table 2).

Percent relative colonization was much higher than percent relative extinction at stand scale in all *Brachypodium* types from 1993 to 1994, but relative colonization and extinction balanced from 1994 to 1995, except the Forest-steppe type. Similar tendency was apparent at microquadrat scale, as well.

Stand-scale relative turnovers (Table 3A) varied between 31% and 58%, while average relative local turnovers (Table 3B) were much higher ranging between 85% and 102% at microquadrat-scale, indicating intensive fine-scale dynamics from year to year. Although the changes of relative turnover showed rather fluctuation at stand-scale, but local species turnover changed at micro-scale showed a slightly increasing tendency from forest to steppe types of *Brachypodium* grassland (Tables 3A and 3B).

Table 2. Species richness at stand-scale and average species number and percent number of 5 cm x 5 cm gaps estimated at microquadrat-scale

	1993			1994			1995		
	Forest-type	Forest-steppe-type	Steppe-type	Forest-type	Forest-steppe-type	Steppe-type	Forest-type	Forest-steppe-type	Steppe-type
Total number of species / 5.5 m^2	50	57	46	61	67	61	62	63	59
Average number of species / 0.0025 m^2	1.72	2.13	1.07	2.09	2.38	1.31	2.08	2.50	1.34
Percent number of 25cm^2 gaps/5.5 m^2	7.7	8.6	10.5	3.8	4.8	6	4	4.8	5.5

Table 3. Plant colonization and turnover changes in three Brachypodium types over three years
A: Colonization is the number of newly appearing species between subsequent years and extinction is the number of disappeared species between subsequent years within a stand (study area is 5.5 m2). Relative colonization % is the ratio of the number of species appearing in the microquadrats (2200) in a year (t) and the total number of species present in that year (t). relative extinction % is expressed as the number of species disappearing from all microquadrats of a stand between year (t-1) and year (t), divided by the total number of species present in the year (t-1).
B: Average local turnover and average local colonization and extinction estimated at microquadrat-scale. Average relative local turnover is calculated as local species turnover per number of species of the microquadrats in the second year.

A)

Stand-scale (5.5 m^2)	1993-1994			1994-1995		
	Forest-type	Forest-steppe-type	Steppe-type	Forest-type	Forest-steppe-type	Steppe-type
Turnover	19	30	29	27	24	34
Relative turnover (%)	31	44	47	44	38	58
Colonization	15	20	22	14	10	16
Extinction	4	10	7	13	14	18
Relative colonization (%)	25	30	36	23	16	27
Relative extinction (%)	8	20	15	21	21	30

B)

Microquadrat-scale (0.0025 m^2)	1993-1994			1994-1995		
	Forest-type	Forest-steppe-type	Steppe-type	Forest-type	Forest-steppe-type	Steppe-type
Average local turnover	1.8	2.1	2.04	1.83	2.20	2.21
Average relative local turnover (%)	85.9	90.59	90.88	88.43	91.36	101.79
Average local colonization	1.08	1.17	1.17	0.91	1.16	1.08
Average local extinction	0.72	0.92	0.87	0.92	1.04	1.12

Within-stand patterns of local species turnovers (significance of contagion indices)

Local temporal dependence

Significant temporal contagion indices obtained for all *Brachypodium* types indicated that the local species turnovers between subsequent years were not independent from each other. It meant that e.g. the micro-quadrats of slow species exchanges were relatively constant in time.

Local spatial dependence

Significant spatial dependence of local species turnovers between spatially adjacent micro-quadrats was revealed in the Forest- and Forest-steppe types in each year: small localities with similarly low or high species turnover occurred close to each other. On the contrary, a non-significant spatial contagion was found in the Steppe-type, which showed a decreasing spatial dependence in this type.

Vegetation pattern vs. local species turnover

Plexus diagrams (Fig. 1) depicted the significant spatial associations between spatial patterns of 3 grasses and patterns of localities with high/low local species turnovers.

Significant positive spatial associations between species turnovers of the subsequent years showed that the patterns of local turnovers were not independent in time (cf. local temporal contagion indices). Many significant spatial associations between spatial patterns of particular species and turnover patterns indicated that the local species exchanges were influenced by the spatial pattern of existing vegetation as well, and inversely the spatial vegetation patterns were generated by the patterns of turnovers. Although, the significant associations did not appear in every year, we do not think that the revealed correlations would change considerably during a short time interval (3 years), but rather, the lack of significant associations could be induced by the changes of species abundances and interspecies competition. Therefore, in the interpretation of

results we accepted a significant value if there was at least one year with significant value.

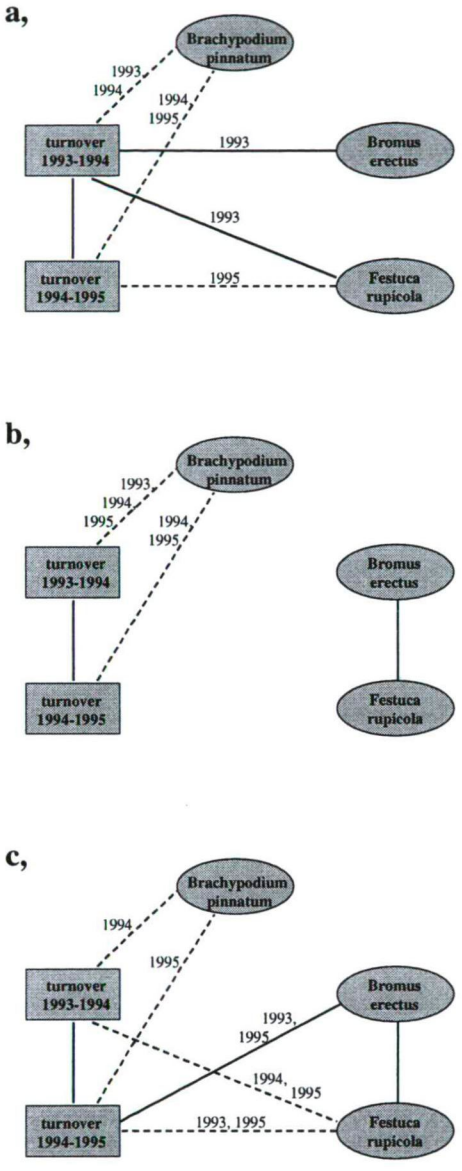

Figure 1. Plexus diagrams depicting the spatial associations between the patterns of three grasses and the patterns of high/low local species turnovers. a: Forest-type, b: Forest-steppe type, c: Steppe-type. _____ significant positive associations, -------- significant negative associations

In the Forest-type (Fig. 1a) significant spatial associations were found between the spatial patterns of three dominant grasses and the spatial patterns of local species turnovers. Our results suggested that *Brachypodium pinnatum* "decelerated", while the subordinate—rare *Festuca rupicola* and *Bromus erectus* "accelerated" the turnovers in this vegetation type.

Spatial patterns of *Bromus erectus* and *Festuca rupicola* were not correlated with the turnover patterns in the Forest-steppe-type (Fig. 1b). Here numerous dicots might also be responsible for the degree of turnovers (see Virágh and Bartha 1998c). *Brachypodium pinnatum* showed negative associations with the temporal species turnovers.

In the Steppe-type (Fig. 1c) both *Brachypodium pinnatum* and *Festuca rupicola* revealed negative relationships with the turnover patterns. Only the spatial pattern of *Bromus erectus* was correlated positively with the relative species exchanges. There was a positive significant association between spatial patterns of *Bromus erectus* and *Festuca rupicola*, indicating that these species could co-occur in this patch and also in the Forest-steppe type. However, these species could not coexist with *Brachypodium pinnatum* in any of the patches.

Discussion

Species turnover in different types of Brachypodium pinnatum grassland

The changes of species richness and relative turnover % showed rather fluctuation at stand-scale in each *Brachypodium* type over three years. Average relative local species turnover was very high at microquadrat-scale, indicating a slightly increasing tendency from forest to steppe types of *Brachypodium* grassland. Closed canopy vegetation gradually opened and microheterogeneity increased, all induced increasing intensity of local species turnover towards more xeric *Brachypodium* types. These may indicate that multilayered *Brachypodium pinnatum* stand canopy involved a highly competitive environment with high relative local species exchanges and spatial differentiation at microquadrat-scale (cf. Bartha *et al.* 2003, Virágh and Bartha 1998a). Strong fine-scale spatial differentiation among species into contrasting species coalitions according to *Brachypodium* types had been pronounced by previous studies (Virágh and Bartha 1998a, Virágh et al 2000). We also suggest that more intensive fine-scale turnover dynamics from Forest-type to Steppe-type may be principally influenced by a gradual decline of abundance—dominance of *Brachypodium pinnatum*, associated with changes of abundance shift among species and spatial organization of individuals, as well as coincided with varying light conditions and decreasing canopy height and litter thickness.

Plant colonization changes over three years

It was clear that colonization and average local colonization were the highest between 1993 and 1994, while extinction and average local extinction were between 1994 and 1995, in all *Brachypodium* types.The number of gaps decreased over three years. If we inspected the annual total precipitation (341 mm in 1992, 493 mm in 1993, 482 mm in 1994 and 637 mm in 1995) and considered the years 1993 and 1994 as extreme dry and the year 1995 as strongly wet according to the 13-year precipitation average (554.6 mm) in the study site, we could take some speculation on the role of climatic feature for vegetation dynamics. We thought that as our investigation was started in an exceptionally dry year (1992), thus the decreasing speed of species colonization, increase in extinction from 1993 to 1995, as well as decrease in gap availability during following years could be interpreted as a post-drought dynamics. The drought caused damage to the vegetation, created the openings, so the current study showed how during 1993 and 1995 the vegetation recovered.

Within-stand patterns of vegetation and local species turnover

Our results showed that local species turnover patterns were temporally and spatially non-random in our spatially heterogeneous *Brachypodium* grassland types. High and low local species turnovers were dependent on the spatial structure of vegetation. Spatial behaviours of some matrix-forming grass species controlled the fine-scale species turnover patterns.

Recently many papers (Rusch and van der Maarel 1992, van der Maarel and Sykes 1993, Herben *et al.* 1993, 1994, Fröborg and Eriksson 1997, Klimes 1999, Palmer and Rusch 2001) had focused on spatial mobility of particular species at different scales and its underlying mechanisms (Otsus and Zobel 2002, Tamm *et al.* 2002, Sammul *et al.* 2003). Most of them emphasized that species mobility was shown to vary individualistically (e.g. van der Maarel and Sykes 1993), however, few studies had already pointed to the importance of spatial dynamics of whole community for influencing strategies of spatial exploitation of particular species or turnover rates of all constituent species (e.g. Otsus and Zobel 2002).

Relative role of matrix-forming grass species in controlling local species turnover patterns

Comparing the relative role of three key grass species we can state that the species differed from structuring the patterns of local turnovers in *Brachypodium* patches.

The dominant clonal *Brachypodium pinnatum* decelerated fine-scale turnovers in all types, as the relationships between patterns of occurrences of this species in the microquadrats and the spatial patterns of high local species turnovers were significantly negative.

On the contrary, the local species exchanges of microquadrats including *Bromus erectus* were always high. Spatial behaviour of this species, however, differed in *Brachypodium* types of contrasting coenological structure and spatial microheterogeneity. *Bromus erectus*, as a rare species with low cover in the Forest-type, most frequently occurred in the gaps within the dense clonal architecture of predominant *Brachypodium pinnatum*, where in the gaps there were always the highest species mobility due to some gap-exploiter species mainly propagateing by seeds and where the vegetative appearances of *Brachypodium pinnatum* also accounted for increasing the rate of local temporal turnovers. Seeds of *Bromus erectus* only dispersed from the species pool of near neighbours into this vegetation type, as the individuals never reached their mature phase with producing seeds within this community. In the Forest-steppe and Steppe-type this species was codominant due to spreading successfully both by vegetatively and generatively. It showed significant positive spatial associations with many graminoids and dicots (see Virágh and Bartha 1998), but its well-developed individuals (clumps) did not prevent newly appearances of other species, either. In the Steppe-type where the key grasses were spatially segregated in the open canopy of vegetation, *Bromus erectus* had a great success in exploiting open spaces by vegetatively or mainly by generatively, as well as it also allowed local colonization of many other dicots into microquadrats dominated by itself.

Festuca rupicola both accelerated and decelerated local turnovers. *Festuca rupicola* also appeared in the small openings of the dense stand predominated by *Brachypodium pinnatum* in the Forest-type, and as a low-frequent species accelerated local species turnovers, similarly to *Bromus erectus*. Nevertheless, when frequency of *Festuca rupicola* increased by 20 - 30 % in this patch (1995), it could decelerate local species exchanges, as well. Fine-scale spatial patterns of *Festuca rupicola* could be considered relatively stabile in Steppe-type, where it frequently occupied the same places from year to year and limited appearances of other species. Hence, *Festuca* decelerated local species dynamics, such as *Brachypodium pinnatum* did.

We also emphasized here that the same species had different fine-scale spatial behaviours according to their abundances and hence they could have different roles in generating local species turnovers in vegetation types of contrasting spatial organizations and fine-scale coexistence structures. Role of species with similar propagating strategies, such as *Bromus erectus* and *Festuca rupicola* with limited clonal growth, was different in influencing fine-scale turnovers, or inversely, other species of different growth forms and propagating strategies, such as *Brachypodium pinnatum* with extensive clonal growth and *Bromus erectus*, behaved similarly in generating slow local species turnovers in certain coenological conditions. Such like conclusions merged from the studies by Herben *et al.* (1993) and also Klimes (1999), when fine-scale spatial dynamics of individual species and its correlation with plant growth form were investigated.

Thus, answering our first questions posed in the introduction, we can say, that in the *Brachypodium* grassland types developing after clear-felled oakwoods, local species turnovers were principally constrained by the abundance and dominance relationships among species and also influenced by the canopy height and closure. Referring to the second question we can conclude that the fine-scale species turnover patterns were temporally and spatially non-random. High and low local species turnovers depended on spatial structure of vegetation. As to the third question, we suggest that some matrix grass species had important roles in structuring the local species turnover patterns, according to their abundances. Their spatio-temporal behaviours were not specific but influenced by the microcoenological structure and spatial organization of the whole community.

As our study revealed close relationships between spatio-temporal changes of local species turnover and spatial patterns of three matrix-forming grass species, therefore we suggest that fine-scale species turnover is not only a phenomenon but is a function of vegetation pattern and it is also a mechanism which generates spatial structure of vegetation. Still, we also think that much more similar analyses may be necessary to make comparisons between many types of communities, which can also promote a further synthesis on vegetation dynamics characterized by species turnover as a working mechanism, dependent on vegetation pattern.

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TISCIA 34, 57-60

Short communication

GROWTH OF THE MUDMINNOW (*UMBRA KRAMERI* WALBAUM) IN RIVER ÉR

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Wilhelm, A. (2003): Growth of the mudminnow *(Umbra krameri* Walbaum) in river Ér. – *Tiscia 34, 57-60.*

Abstract. Growth characteristics of the mudminnow were studied in river Ér on the basis of length and weight measurements of 252 individuals. Relationship between body length and weight was determined and the expected growth of the length was calculated with the Walford and Bertalanffy methods. Our results were compared with data of Slovakian populations.

Keywords: Bertalanffy model, body length, body weight, Walford method

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Introduction

The mudminnow is an endemic fish species of the rivers Danube and Dniester. It is a typically stagnophyl species and its population has significantly decreased in the last decades, therefore Maitland (1991) considers it a highly endangered species. Bănărescu (1993, 1994) points out that the mudminnow becomes frequent in places where it finds suitable circumstances. The protection of moors, slow, muddy small rivers and brooks with certain vegetation would solve the survival of this species.

The growthof the individuals of the European mudminnow population has been studied by many researchers, but no detailed study suitable for comparison have been published. The first data were published by Geyer (1940) from the territory of Hungary, but he stated that the species could reach only the age of two years. Pavlov (1953) mentioned about the age of 5-6 from the lower reaches of the Danube, and he found larger sizes compared with those of Geyer. Based on these data, Kux and Libosvárský (1957) described two subspecies (*Umbra krameri karmeri* and *U. krameri pavlovi*) in the Lower Danube and Middle Europe, but later this was revised (Baruš and Libosvárský 1983).

Most of the studies about the growth of the mudminnow were published in Slovakia (Libosvárský and Kux 1958, Mišik 1966, Makara and Stráňai 1980), but these consider only the age of two years. Growth studies of the mudminnow population in the Ér Valley (Wilhelm 1984, 1987) showed that this fish can reach the age of six.

Comparative data about the growth of the mudminnow were published by Wanzenböck (1995).

Material and methods

252 mudminnow individuals were gathered between 1973 and 1995 with a scratching net. I measured total length (Lt), standard length (Lc) (without the caudal fin) and body weight (W) of the fishes.

The age of the specimens was determined from the annual rings of the scales previously treated with a solution of 0.2 % NaOCl with a trichinoscope, and later with a stereomicroscope.

In the description of the growth of length I used the values of the standard length, but in some countries the total length is used, so I determined the equation of the transformation of the standard to total length using the following formula:

$Lt = bLc + a$

The relationship between the body length and weight was determined with the formula of Tesch (1968):

$W = aL^b$

based on the standard and total length too, where "a" is the regression coefficient and "b" has a value of approximately 3.0.

For the mathematical description of the growth I used the Walford (1946) method and the Bertalanffy (1957) model.

Standard length of age group "t+1" was plotted against that of age group "t" and the Walford linear plot was calculated

$L_{t+1} = a + bL_t$.

The X value of the point of the intersection of the Walford plot and the diagonal of 45° is the maximum theoretically achievable (asymptotic) length (Lc_{inf}).

According to the Bertalanffy model, the length achieved at any "t" time can be calculated with the following formula:

$Lc_t = Lc_{inf}[1 - e^{-K(t - t_0)}]$,

where "K" is the growth constant, t_0 is a hypotethical moment when the length is zero, "e" is the basis of the natural logarithm. I plotted $\ln(Lc_{inf} - Lc_t)$ against the age and the value of "K" was determined from

$y = a - Kx$

To calculate the value of t_0, I put on the Y axis the value of $\ln Lc_{inf}$ and draw a parallel with the X axis. The X value of the point of intersection of this parallel with the initial regression line is the t_0. The value of t_0 can be calculated with the formula:

$t_0 = (\ln Lc_{inf} - a) / b$,

where "a" and "b" are the constants of the regression line. The exact value of Lc_{inf} can be calculated using the following formula:

$Lc_{inf} = a / (1 - b)$

The condition of the fish was calculated using the formula:

$CF = W / Lc^b$

where "b" corresponds to the "b" value from the formula of the relationship between the body weight and standard length. I used the average values of the standard lengths of the different age groups in mm and the average weights in g.

Results

Table 1. The mean standard and total body length and average weight values belonging to the different age groups

Age	Standard length (mm)	Total length (mm)	Weight (g)
0+	38.4 ± 1.4	48.3 ± 2.0	1.05 ± 0.12
1-1+	44.2 ± 2.6	55.4 ± 2.9	1.57 ± 0.27
2-2+	50.6 ± 2.9	63.0 ± 3.5	2.27 ± 0.47
3-3+	57.4 ± 3.9	70.4 ± 2.4	3.35 ± 0.56
4-4+	67.9 ± 5.8	82.0 ± 5.9	5.77 ± 1.52
5-5+	76.9 ± 5.0	91.5 ± 3.1	8.51 ± 1.47
6-6+	88.1 ± 7.6	105.5 ± 9.0	16.49 ± 6.21

The standard length (Lc) of the fishes varied between 38 and 88 mm, the total length was between 48 and 105 mm, and their weight between 1 and 16.5 g (Table 1). The relationship between standard and total length is:

$Lt = 0.8764Lc - 4.3436$ $(R2 = 0.9811)$.

The distribution of the collected fish exemplars of different ages according to their standard length is shown in Table 2.

Table 2. Distribution of the collected specimen according to their standard length and age

Age	0+	1-1+	2-2+	3-3+	4-4+	5-5+	6-6+	7-7+
standard length								
35.5-40	13	4						
40.5-45	1	47	3					
45.5-50		38	39					
50.5-55			41	7				
55.5-60			6	19	1			
60.5-65				2	3			
65.5-70				1	5			
70.5-75					4	4		
75.5-80					1	5		
80.5-85							2	
85.5-90						1	3	1
90.5-95								
95.5-100								
100.5-105								
105.5-110							1	

I determined the equation of the relationship between (total and standard) length and weight (Figs 1 and 2).

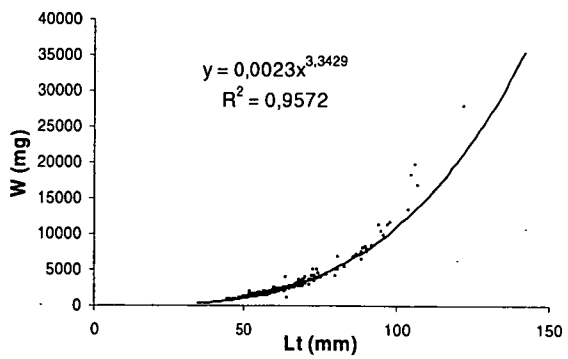

Fig. 1. The exponential relationship between total length and weight

According to the Walford model the maximum achievable (asymptotic) length proved to be 84.20 mm (Fig. 3).

The equation of the regression plot used for the determination of the t_0 and "K" value of the Bertalanffy model was (Fig. 4):

$y = -0.3458x + 4.3927$

$t_0 = -0.1168$

$K = -0.3458$.

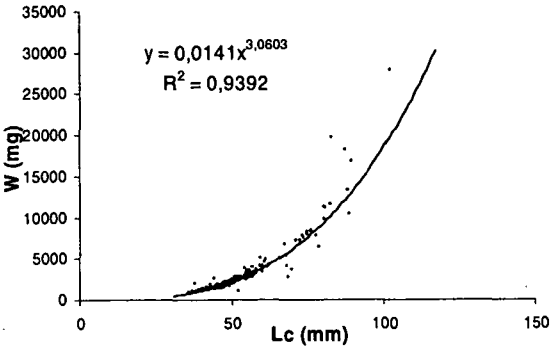

Fig. 2. The exponential relationship between standard length and weight

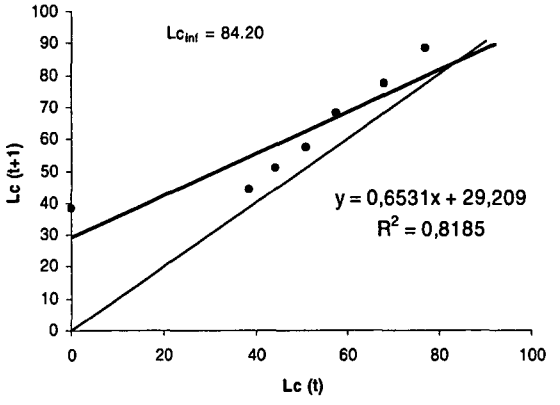

Fig. 3. The growth of the mudminnow according to the Walford model

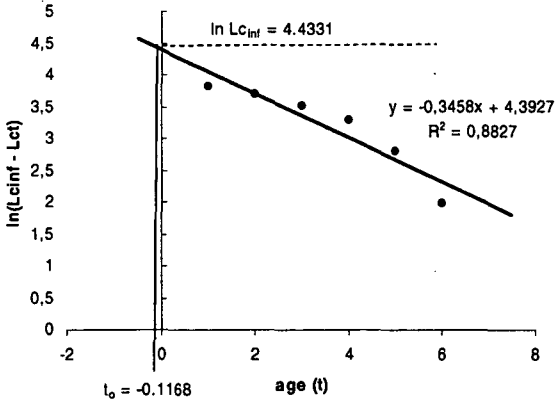

Fig. 4. Determination of the parameters (t_0 and K) of the Bertalanffy equation

The growth of the mudminnow according to the Bertalanffy model is shown in Fig. 5. The equation of the plot is:

$$Lc_t = 84.2[1 - e^{0.3458(t + 0.1168)}]$$

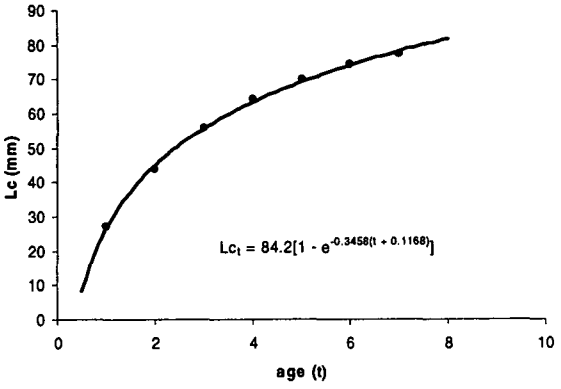

Fig. 5. Growth of the mudminnow according to the Bertalanffy model

The comparison between the measured standard lengths and the calculated lengths according to the Walford and the Bertalanffy model respectively is presented in Table 3.

Table 3. Body length data based on the measurements taken and calculated by the Walford model and the Bertalanffy method

	Standard length (mm)		
Age	Measurement	Walford model	Bertalanffy model
0+	38.4	29.2	26.9
1-1+	44.2	54.3	43.7
2-2+	50.6	58.1	55.5
3-3+	57.4	62.3	63.9
4-4+	67.9	66.7	69.8
5-5+	76.9	73.6	74.0
6-6+	88.1	79.4	77.0

The condition of the different age groups is presented in Table 4.

Table 4. The condition of the different age groups

Age	Condition
0+	0.0000148
1-1+	0.0000144
2-2+	0.0000137
3-3+	0.0000138
4-4+	0.0000142
5-5+	0.0000143
6-6+	0.0000183
Mean	0.0000148

Discussion

The "b" constant of the equation of the standard length—weight relationship is approximately 3 when the growth of the length and weight is uniform ("isometric") (Bíró 1993). In our case this value is 3.0603, which means that the weight grows faster than the length. Mišik (1966) considers that "b"

value refers to the feeding conditions of the population. The value above 3 indicates that in the river Ér the nutritional conditions are satisfactory for the mudminnow. My results are similar to the observations of Kux and Libosvárský (1958) and Mišik (1966) from Slovakia, which varied between 2.935 and 3.206.

Comparing the measured data with the values of Walford and Bertalanffy models, note that the measured lengths in the one-year and five-six-year age groups exceed those calculated with the models. The cause of the previous can be the rapid growth of the fish in the first year, and since the collected material comes from different months of the year, there can appear significant differences in the size. The latter one can be explained with the decreased reproduction of the older individuals.

The condition of the fish changes with the age: from the starting values of the first-year individuals it decreases in the case of the reproducing age groups and then increases again in the older age groups less involved in the reproduction.

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